

WEST Search History

DATE: Thursday, May 27, 2004

Hide?	Set Name	Query	Hit Count
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L12	L9 .clm.	26
<input type="checkbox"/>	L11	L9 adj number	0
<input type="checkbox"/>	L10	L9 and l3	477
<input type="checkbox"/>	L9	209526	517
<input type="checkbox"/>	L8	Accession number 2090526	0
<input type="checkbox"/>	L7	wood-william-\$.in	0
<input type="checkbox"/>	L6	wood-william-\$.in	0
<input type="checkbox"/>	L5	gurney-austin-\$.in.	1827
<input type="checkbox"/>	L4	godowaski-paul-\$.in.	0
<input type="checkbox"/>	L3	goddard-audrey.in.	1871
<i>DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L2	Fivaroff-ellen.in.	0
<input type="checkbox"/>	L1	6642360.pn.	1

END OF SEARCH HISTORY

[First Hit](#) [Fwd Refs](#)**End of Result Set**☐ **Generate Collection** **Print**

L1: Entry 1 of 1

File: USPT

Nov 4, 2003

US-PAT-NO: 6642360

DOCUMENT-IDENTIFIER: US 6642360 B2

TITLE: Secreted polypeptides that stimulate release of proteoglycans from cartilage

DATE-ISSUED: November 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Filvaroff; Ellen	San Francisco	CA		
Goddard; Audrey	San Francisco	CA		
Godowski; Paul J.	Burlingame	CA		
Grimaldi; J. Christopher	San Francisco	CA		
Gurney; Austin L.	Belmont	CA		
Wood; William I.	Hillsborough	CA		

US-CL-CURRENT: 530/350; 530/324

CLAIMS:

What is claimed is:

1. An isolated polypeptide having at least 80% amino acid sequence identity to: (a) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2); (b) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2), lacking its associated signal peptide; or (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209526; wherein the polypeptide is able to stimulate release of proteoglycans from cartilage.

2. The isolated polypeptide of claim 1 having at least 85% amino acid sequence identity to: (a) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2); (b) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2), lacking its associated signal peptide; or (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209526; wherein the polypeptide is able to stimulate release of proteoglycans from cartilage.

3. The isolated polypeptide of claim 1 having at least 90% amino acid sequence identity to: (a) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2); (b) the amino acid sequence of the polypeptide shown in FIG. 2 (SEQ ID NO:2), lacking its associated signal peptide; or (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209526; wherein the polypeptide is able to stimulate release of proteoglycans from cartilage.

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L1: Entry 1 of 1

File: USPT

Jan 28, 2003

US-PAT-NO: 6512095

DOCUMENT-IDENTIFIER: US 6512095 B2

TITLE: Molecules designated B7L-1

DATE-ISSUED: January 28, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Baum; Peter R.	Seattle	WA		

US-CL-CURRENT: 530/350; 424/130.1, 424/133.1, 424/134.1, 424/184.1, 424/185.1,
424/192.1, 424/193.1, 530/387.1, 530/387.3, 530/395

CLAIMS:

What is claimed is:

1. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
2. The isolated polypeptide of claim 1, wherein x.sub.1 is 21.
3. A composition comprising: an isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21, and an agent selected from the group consisting of a therapeutic drug, a toxin, a radionuclide, a chromophore, a colorimetric molecule, and a fluorometric molecule, wherein the agent is linked to the polypeptide.
4. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the nucleotide sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1.
5. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
6. The fusion polypeptide of claim 5, wherein x.sub.1 is 21.
7. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

8. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transfected or transformed with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1,

under conditions such that the polypeptide is produced from the DNA.

9. The polypeptide of claim 8, wherein x.sub.1 is 157.

10. The polypeptide of claim 8, wherein x.sub.1 is 217.

11. The polypeptide of claim 8, wherein the method further comprises recovering the polypeptide.

12. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the sequence as set forth in SEQ ID NO:4; and (b) a polypeptide comprising the sequence from about x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

13. The isolated polypeptide of claim 12, wherein x.sub.1 is 21.

14. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the sequence from nucleotide x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73.

15. The isolated polypeptide of claim 14, wherein the DNA comprises the sequence as set forth in SEQ ID NO: 3.

16. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

17. The fusion protein of claim 16, wherein the fusion polypeptide comprises the sequence as set forth in SEQ ID NO:4 from amino acid 21 to amino acid 330.

18. The fusion polypeptide of claim 16, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

19. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transformed or transfected with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the nucleotide sequence x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73,

wherein the host cell is cultured under conditions such that the polypeptide is produced from the DNA.

20. The polypeptide of claim 19, wherein x.sub.2 is 13.

21. The polypeptide of claim 19, wherein x.sub.2 is 73.

22. The polypeptide of claim 19, wherein the method further comprises recovering the polypeptide.
23. A composition comprising a suitable carrier and a polypeptide of claim 1.
24. A composition comprising a suitable carrier and a polypeptide of claim 12.
25. A composition comprising a suitable carrier and a fusion polypeptide of claim 5.
26. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to X2 of SEQ ID NO: 2 having one amino acid deletion, insertion or substitution thereto, wherein x.sub.1 is 1 or 21 and x.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a sequence as set forth in SEQ ID NO: 20 or 22.
27. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to x.sub.2 of SEQ ID NO: 2 having a deletion of 1 to 5 terminally located amino acids, wherein x.sub.1 is 1 or 21 and X.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a

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End of Result Set

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L1: Entry 1 of 1

File: USPT

Jan 28, 2003

US-PAT-NO: 6512095

DOCUMENT-IDENTIFIER: US 6512095 B2

TITLE: Molecules designated B7L-1

DATE-ISSUED: January 28, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Baum; Peter R.	Seattle	WA		

US-CL-CURRENT: 530/350; 424/130.1, 424/133.1, 424/134.1, 424/184.1, 424/185.1,
424/192.1, 424/193.1, 530/387.1, 530/387.3, 530/395

CLAIMS:

What is claimed is:

1. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
2. The isolated polypeptide of claim 1, wherein x.sub.1 is 21.
3. A composition comprising: an isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the amino acid sequence as set forth in SEQ ID NO:2; and (b) a polypeptide comprising amino acids x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21, and an agent selected from the group consisting of a therapeutic drug, a toxin, a radionuclide, a chromophore, a colorimetric molecule, and a fluorometric molecule, wherein the agent is linked to the polypeptide.
4. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the nucleotide sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1.
5. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 364 of SEQ ID NO:2, wherein x.sub.1 is 1 or 21.
6. The fusion polypeptide of claim 5, wherein x.sub.1 is 21.
7. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

8. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transfected or transformed with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:1; (b) a DNA comprising the nucleotide sequence from x.sub.1 to 1452 of SEQ ID NO:1, wherein x.sub.1 is 157 or 217; and (c) a DNA comprising the nucleotide sequence from 108 to 1249 of SEQ ID NO:1,

under conditions such that the polypeptide is produced from the DNA.

9. The polypeptide of claim 8, wherein x.sub.1 is 157.

10. The polypeptide of claim 8, wherein x.sub.1 is 217.

11. The polypeptide of claim 8, wherein the method further comprises recovering the polypeptide.

12. An isolated polypeptide selected from the group consisting of: (a) a polypeptide comprising the sequence as set forth in SEQ ID NO:4; and (b) a polypeptide comprising the sequence from about x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

13. The isolated polypeptide of claim 12, wherein x.sub.1 is 21.

14. An isolated polypeptide encoded by DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the sequence from nucleotide x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73.

15. The isolated polypeptide of claim 14, wherein the DNA comprises the sequence as set forth in SEQ ID NO: 3.

16. A fusion polypeptide comprising the amino acid sequence from x.sub.1 to 330 of SEQ ID NO:4, wherein x.sub.1 is 1 or 21.

17. The fusion protein of claim 16, wherein the fusion polypeptide comprises the sequence as set forth in SEQ ID NO:4 from amino acid 21 to amino acid 330.

18. The fusion polypeptide of claim 16, wherein the fusion polypeptide comprises an Fc region and/or a peptide linker.

19. A polypeptide produced by a method comprising culturing a recombinant host cell that has been transformed or transfected with a DNA selected from the group consisting of: (a) a DNA comprising the sequence as set forth in SEQ ID NO:3; and (b) a DNA comprising the nucleotide sequence x.sub.2 to 1206 of SEQ ID NO:3, wherein x.sub.2 is 13 or 73,

wherein the host cell is cultured under conditions such that the polypeptide is produced from the DNA.

20. The polypeptide of claim 19, wherein x.sub.2 is 13.

21. The polypeptide of claim 19, wherein x.sub.2 is 73.

22. The polypeptide of claim 19, wherein the method further comprises recovering the polypeptide.
23. A composition comprising a suitable carrier and a polypeptide of claim 1.
24. A composition comprising a suitable carrier and a polypeptide of claim 12.
25. A composition comprising a suitable carrier and a fusion polypeptide of claim 5.
26. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to X2 of SEQ ID NO: 2 having one amino acid deletion, insertion or substitution thereto, wherein x.sub.1 is 1 or 21 and x.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a sequence as set forth in SEQ ID NO: 20 or 22.
27. An isolated polypeptide comprising a B7L-1 variant consisting of a sequence as set forth from x.sub.1 to x.sub.2 of SEQ ID NO: 2 having a deletion of 1 to 5 terminally located amino acids, wherein x.sub.1 is 1 or 21 and X.sub.2 is 364 or 432, and wherein the B7L-1 variant is capable of binding a LDCAM polypeptide having a

Db 242 YPEVVIS-GYDNNWYLQNEA-TLTCDA RSNPEPTGYNWSTTMGLPPLPPFAVQAQALLI 299
Qy 283 NNLAKTNDGTGYRCEASNTVGKAHSDYMLYVYDPPPTIPPTTTTTTTTTTTTTTTTTIITD 342
Db 300 RPVDKPTNTTLCVNTNAGARQELTVQVE-----GPPSEHS----- 338
Qy 343 SRAGEEGTIGAVDHAVIGGVAVVVFVAMCLLIILGRYF 381
Db 339 -----GMSRNAIFLVLGILVF---LILLGIGIVF 365

RESULT 14
156551
neurotrimin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C/Accession: I56551
R/Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Reesen, C.L.; D'Eustachio, P.; Salzer, J.L.
J. Neurosci. 15, 2141-2156, 1995
A/Title: Cloning of neurotrimin defines a new subfamily of differentially expressed neu
A/Reference number: I56551; MUID:95198094; PMID:7891157
A/Accession: I56551
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-344 <RES>
A/Cross-references: EMBL:U16845; NID:9755184; PIDN:AAAC7445.1; PID:9755185
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 10.5%; Score 231; DB 2; Length 344;
Best Local Similarity 26.2%; Pred. No. 5.1e-09;
Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

Qy 10 LLLLLLSAAALIPG-----DGNLFK---DVTVIEGEVATISQVNVKSDSDSVIQLNPN 62
Db 14 LVVSLRLLELVPTGVPVRSQDATPPKAMDNVTVRQGESATLRCTI---DNRVTFVAVLN 70

Qy 63 RQTI-YFRDFRPLKDSRQLLNFSSELKSLTNVVISDEGRYFCQLYTD-PPQESYTTI 120
Db 71 RSTILYAGNDKWCIDPRVLLSNTQYISIEIQNVVYDEGPTQCSVQTDNHPKTSRVHL 130

Qy 121 TVLPPRNLMDIQDQAV-EGEIEVNCTAMASKPATTIRWFKGNKELKKGSEVWSD 179
Db 131 IVQVSPK--IVEISSDISINGNNISLFCIA-TGRPEPTVTRHISPAVGFVSEDEYLE 187

Qy 180 MYTVTSQMLKLVH---KEDDGPVVICQVEHPAVTGNLTQRYLEVQYKPVQVHIQMTYPLQ 236
Db 188 IQGITREQSGEVECSASNDVAAPVVRVN-----VTWVPPYIS---EAK 229

Qy 237 GL-TREGDAFELTCEATGKQPQVMTVVRVDEMPQ-----HAVLSGNLFINNLM 286
Db 230 GTGVFVGQKGTQCEASAVPS-ABFQWPKDDKRLVEGKGVKVENRPFSLRLTFF--NVS 286

Qy 287 KTDNGTYRCEASNTVGKAHSDYMLY 311
Db 287 EHDYGNVTCVASNKLGHNTNASIMLF 311

RESULT 15
I38346
elastic titin - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: I38346
R/Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A/Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A/Reference number: A57430; MUID:96026330; PMID:7569978
A/Accession: I38346
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-7962 <RES>
A/Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427
C/Genetics:

A/Gene: GDB:TTN
A/Cross-references: GDB:127867; OMIM:188840
A/Map position: 2q31-2q31

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Best Local Similarity 26.1%; Pred. No. 4e-07;
Matches 80; Conservative 55; Mismatches 130; Indels 41; Gaps 13;

Qy 35 TVIRGEVATISQVNVKSDSDSVIQ---LLN-----PNRQTIYFRDFRPLKDSRFQLLNPF 84
Db 770 TVLDRDIAPFTKPLRNVDVSVNGTCLDCKIAGSLPMRVS-WFKDGKRIAAADRYRIAF 828

Qy 85 SSSELKVLNTNVSISDEGRYFCQLYTD-PPQESYTTITVLVPPRNLMDIQDQAVEGEE 143
Db 829 VEGTASLEIIRVDMNDAGNFTCRATNSVGSKDSSGALIVQEPFVFKPGSKD-VLPESA 887

Qy 144 IEVNCTAMASKPATTIRWFKGNKELKG-----KSEVEWSDMYTVTSQMLKVKHKEDD 196
Db 888 VCLAKSTFGGSTP-LTIRWFKGNKELVSGGSCYITKEALSSLELYLV-----KTS 937

Qy 197 GVPVICQVEHPAVTGNLTQRYLEVQYKPVQVHIQMTYPLQGLTREGDAFELTCEAIGK 256
Db 938 SGTYTCKVSN--VAGGVECSANLEVK-EPATFVEKLEPSQ-LLKKGDTQLACKVTGTP- 992

Qy 257 PVMTVTVRVDDEMPQHA-----VLSGPNLFINNLTNDNGTYRCEASNTVGKAHSDYML 310
Db 993 PIKITWPFANDREIKESKHRMSFVESTAVLRITDVGIEDSGEYVCEAQNAGSDHCSSIV 1052

Qy 311 VYDPP 316
Db 1053 IVKESP 1058

Search completed: May 27, 2004, 09:32:24
Job time : 13.2283 secs

Db 62 SOLTWRHGGSSGMAVPHOTQGNYPSEKLEFVAARLGTSLRDAASLRMFLRVEDEGNY 121
QY 105 FCOLYTDPPQESYTT---ITVLVPPRLNLMIDIKOTAVEGEEIEV-NCTAMASKPATIIR 160
Db 122 TC-LFVTFPQGSRSVDLWLVAKPN-TAEVQK-VOLTGKPPVAVRCVSTGGRPPAHIT 178
QY 161 WFKGNKELGKSEVEE-----WSDMYTIVTSQMLKVKHEDDGVFVICQVEHPAVTGNLQTO 216
Db 179 W---HSDLGMPNTSQAPGLSGTIVTSLWLVPPSSQVDGKSVTKCKVEHSEPEKQLLT 235
QY 217 RYLEVOYKQVHLOMTYPILOGLTRBGDAFELTCEAIKGPQPMVMTWVRVDDDEMPQHAVLS 276
Db 236 VNLTVYTPPEVSIS-GYDNNWYLSQNEA-TLTCARSNPPTGYNWSTTMGPLPPFAVAQ 293
QY 277 GPNLFINNKNKTNGTYRCASNIIVGKHSYMLVYVDPPTTIPPTTTTTTTTTTTTTTTI 336
Db 294 GAQLLRPVDPKPIINTFICNVNVALGARQALIVQVKEGPPSPS----- 338
QY 337 LTIITDSRAGEGTIGAVDHAVIGVGVVAVFAMLCLLIILGRYFARHKGT----YFTH 392
Db 339 -----GMSNIIIFLILGIVI---LTLTGIGVYFYKRSRCSREFLWCHHL 380
QY 393 AKGADDAADATALINAEQGNNSSEKKE 421
Db 381 SPSEEHASA-----SANGYISYSDVSRE 404

RESULT 10

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Carcophthecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 234.5; DB 2; Length 392;
Best Local Similarity 24.4%; Pred. No. 3 4e-09;
Matches 100; Conservative 58; Mismatches 180; Indels 71; Gaps 16;

QY 1 AADPGLRLRLLLLLSAAALPTGQNLFTKQVTV--IEGEVATISC--QVKNSDSDSVI 56
Db 8 AWPP-----LTLTLELSPPPTGDIIVQAPQVPGFLGDSVTLPCYLQVPMEEHV 61
QY 57 QLLNPNR-----QTIYFRDRLKDSRFQNLNSSFSSSELKSLTNVS-----ISDEGRY 104
Db 62 SOLTWRHGGSSGMAVPHOTQGNYPSEKLEFVAARLGTSLRDAASLRMFLRVEDEGNY 121
QY 105 FCOLYTDPPQESYTT---ITVLVPPRLNLMIDIKOTAVEGEEIEV-NCTAMASKPATIIR 160
Db 122 TC-LFVTFPQGSRSVDLWLVAKPN-TAEVQK-VOLTGKPPVAVRCVSTGGRPPAHIT 178
QY 161 WFKGNKELGKSEVEE-----WSDMYTIVTSQMLKVKHEDDGVFVICQVEHPAVTGNLQTO 216
Db 179 W---HSDLGMPNTSQAPGLSGTIVTSLWLVPPSSQVDGKSVTKCKVEHSEPEKQLLT 235
QY 217 RYLEVOYKQVHLOMTYPILOGLTRBGDAFELTCEAIKGPQPMVMTWVRVDDDEMPQHAVLS 276
Db 236 VNLTVYTPPEVSIS-GYDNNWYLSQNEA-TLTCARSNPPTGYNWSTTMGPLPPFAVAQ 293
QY 277 GPNLFINNKNKTNGTYRCASNIIVGKHSYMLVYVDPPTTIPPTTTTTTTTTTTTTTTI 336
Db 294 GAQLLRPVDPKPIINTFICNVNVALGARQALIVQVKEGPPSPS----- 338

QY 337 LTIITDSRAGEGTIGAVDHAVIGVGVVAVFAMLCLLIILGRYFARHK 385
Db 339 -----GMSNIIIFLILGIVI---LTLTGIGVYFYRSR 369
RESULT 11
IXJNLN
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: EMBL:M25696; NID:G214609; PIDN:AAA49909.1; PID:G214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mo.
C;Comment: Several forms of NCAM are produced by alternative splicing.

C;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LI
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pre
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 1.3e-08;
Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

QY 32 KOVTITEGEVATISC---QVNKS---DDSVIQLLN---PNROTIVFRDPRPLKDSRFQL 81
Db 199 KOIQVIVNVPPTIQARQLRVNATANMAESVLSCDADGFPDEISLWKKEPIEDGE-EK 257
QY 82 LNFSSSELKSLTNVSISEGRYFCOLYTDPPQESYTTITVLVPPRLNLMIDIKOTAVEG 141
Db 258 ISFNDQSESTIHHVKDDAEAYSC-IANNQAGEAEATILLKYAKPKITYVENKTAVEL 316
QY 142 EEIEVNTAMASKPATIIRWFKNGKE-----LACKSEVEESDMYTVTSQMLKXVHE 194
Db 317 DEITLCEA-SGDIPISTWRTAVRNISSEATTLGDHIVVKEHRM---SALTLDKIQY 371
QY 195 DGGVPVICQVEHPAVTGNLQRYLEVQYKQPVHIOQMTYPLQGLTRBGDAFELTCEAIK 254
Db 372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGPNTICEFAH 425
QY 255 PQPMVMTWVRVDDDEMPQ-----AVLSGP---NLFINLNKNTNGTYRCASNIIVGKHS 306
Db 426 PR-AAVTFWRDGLQLPSSNFSNFKIYSGPTSSSLEVPDSEDFGNVCTAINTIGHEFS 484
QY 307 DYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTI 346
Db 485 EFILVQADTFSS---FAIRKVEPYSTVMIVFDEPDSTGG 521

```
QY 329 TTTTTLTITLITDSRAGEGTIGAVDHAVIGGVAVVV 367
Db 344 -----AGAGATGG-----IIGGIIAII 361

RESULT 7
I68093
P:276-331/Domain: immunoglobulin homology <IMM>
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C/Accession: I68093
R/Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A/Title: The human PR2 gene, related to the human poliovirus receptor gene (PVR), is th
A/Reference number: I53960; MUID:95347610; PMID:7622062
A/Accession: I68093
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-538 <RES>
A/Cross-references: GB:S79172; NID:G1042204; PID:G1042205
C/Genetics:
A/Name: PR2delta
C/Superfamily: poliovirus receptor; immunoglobulin homology
F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 238.5; DB 2; Length 538;
Best Local Similarity 22.8%; Pred. No. 2.6e-09;
Matches 110; Conservative 63; Mismatches 196; Indels 113; Gaps 17;

QY 2 APPGLRLLLLSAALIPGTGQMLFTKDVTVIEGEVATISCQVKNKSDSVIQLNP 61
Db 12 SPPTPLLPPLLLL-----LLETG-AQDVRVQVLPVRG-----QLGGTVLPCHLLPP 59
QY 62 -----NRQTIYFRDPRPKDSR-----QLNFSS----- 87
Db 60 VPGYISLVTWQRPDPAHQNV--AAFHPKMGSPFPSPKPSRSLFSVSAKSTGQDTE 117
QY 88 ----ELKVSITNVSISDEGRYFCOLYTDPP--POESYTTITVLVPPRLMIDIQDRTAVEG 141
Db 118 AELQDATLALHGLTVEDEGNVTCBFATFPKSGVRGMLWLVIAKPKN-QAQAQKVTFSQD 176
QY 142 EEIENVCTAMASKPATIRWPKG-NKELKSGEVEWSDMYTTSQMLKLVKHEDDGVV 200
Db 177 PTTVALCISKEGRPPARISLWSSLDWEAKETQVSGTLAGTVTTSRFTLVPSGRADGVTV 236
QY 201 ICQVEHPAVTNLQTRYLEYQKPVQHIQMTYPLQGLTREGDAFELTCEAIGKPPQVMV 260
Db 237 TCKVEHSFEFPALIPVLSVRYPEVSI-S-GYDDNWLGRYDA-TLSCDVRSNPEPTGY 294
QY 261 TWVRVDDMPQHAVLSGNLFINLNKTDNGTYRCEASNIYKRAHSDYMLYVYDPTTIP 320
Db 295 DWSITSGFTFTSAVAQSGQLVIHVDLSLFTFVCTVTNAVGMGRAEQVIVRETPNT-- 352
QY 321 PPTTTTTTTTTTITLITLIDSRAGEGTIGAVDHAVIGGVAVVVVPMCLLIILGRY 380
Db 353 -----AGATGG-----IIGGIIAIIATAVAATGILICR 383
QY 381 PARHKGTYFTHKAGDAADAD-----TALINAE-----GQNNSEKKE 421
Db 384 QORKEQT-----LQAEDEDELGGPPSKPTPKAKLEAQEMPQLFTLGASRSLKTP 438
QY 422 YF 423
Db 439 YF 440

RESULT 8
JE0099
neural cell adhesion molecule 1 - African clawed frog
N/Alternate names: N-CAM 1
C/Species: Xenopus laevis (African clawed frog)
C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: JE0099
R/Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A/Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A/Reference number: JE0099; MUID:98204770; PMID:9535795
A/Accession: JE0099
A/Molecule type: mRNA
A/Residues: 1-725 <KUD>
A/Cross-references: DBJ:AB008162; NID:G3116226; PIDN:BAA25931.1; PID:G3116227
A/Experimental source: heart
C/Comment: This protein mediates and regulates various cell-cell interactions through bo
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F:413-475/Domain: immunoglobulin homology <IMM>
F:512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.8%; Score 238; DB 2; Length 725;
Best Local Similarity 26.2%; Pred. No. 4.2e-09;
Matches 89; Conservative 61; Mismatches 148; Indels 42; Gaps 15;

QY 32 KQVTVIEGEVATISC--QVN---KSDSDSVIQLN---PNRQTIYFRDPRPKDSRFQL 81
Db 159 KDIQVIVNVPPTIQARQLRVNATAKMAESVLSCDADGFPDPEISWLKKGEPEDGE-EK 257
QY 82 LNFSSSELKVSITNVSISDEGRYFCOLYTDPPQESYTTITVLVPPRLMIDIQDRTAVEG 141
Db 258 ISFNEDQSEMTIHVKEKDDAEAYSC-IANNQAGEAEATILLKYAKPKITYVENKTAVEL 316
QY 142 EEEVNTCTAMASKPATIRWPKNGE-----LKGKSEVEWSDMYTTSQMLKLVHKE 194
Db 317 DEITLCEA-SGDIPSITWRTAVRNISSEATLDGHIIVVKEHRM----SALTLDIQY 371
QY 195 DGGVPVICQVEHPAVTNLQTRYLEYQKPVQHIQMTYPLQGLTREGDAFELTCEAIGK 254
Db 372 TDAGEYFCIASNF-IGVDMQAM-YFEVQYAPKIR---GTVVYTWEGNPVNITCEVFAH 425
QY 255 PQVMVTVWVRVDDMPQH-----AVLSGP-----NLFINNLTNGTYRCEASNIYKRAHS 306
Db 426 PR-AAVTFRDGGLPSSNFNISKIYSGPTSSSLEVPDSEDFGNYNCTAINTIGHEFS 484
QY 307 DYMLYVVDPTTIPPTTTTTTTTTTTTTTTTTTTTTITLITDTRAG 346
Db 485 EFTLVQADTFSS---FAIRKVEPYSSTVIMVFDPEPSTGG 521

RESULT 9
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: A44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no puta
A/Reference number: A44194; MUID:93059651; PMID:1331506
A/Accession: A44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-417 <KOI>
A/Cross-references: GB:S48777
C/Superfamily: poliovirus receptor; immunoglobulin homology
C/Keywords: transmembrane protein
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 237; DB 2; Length 417;
Best Local Similarity 23.8%; Pred. No. 2.4e-09;
Matches 107; Conservative 68; Mismatches 194; Indels 80; Gaps 18;

QY 1 AAPGLRLRLLLLSAALIPGTGQNLFTKDVTV--IEGEVATISC--QVKNKSDSVI 56
Db 8 AWPP-----LLLTLELSWPPPGTGDIIVQAPQVPGFLGSDSVTLPCYLQVPGMEETHV 61
QY 57 QLQNPENR-----QTIYFRDPRPKDSRFQLNFSSELKVSITNVS-----ISDEGRY 104
```

F:375-467/Domain: intracellular #status predicted <INT>
 F:54-131,174-229,274-320/disulfide bonds: #status predicted
 F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 246.5; DB 1; Length 467;
 Best Local Similarity 21.6%; Pred. No. 68-10;
 Matches 101; Conservative 72; Mismatches 196; Indels 99; Gaps 16;

QY 4 PGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEV---ATISQV-----48
 DB 14 PTLPLPLLLLL---LQETG-AQDVVRVLPEVGRGLGTGTPCHLLPPTTVERVSQVT 68
 QY 49 -NKSDSVTQLNPNKQTYFRDRLPKDSRQL-----LNFSSSELKSLTNVSIS 99
 DB 69 WORLDGTVAFAHPS---FGVDFPNSQFSKORLSFVRARPETNADLRDATLAFRGLRVE 124
 QY 100 DGRYFCOLYTOP--POESVTTITVLVPRNLMIDIKQDAVEGEIEV-----NCT 149
 DB 125 DGNVTCFATPENGTRGVTWLRVIAQEN-----HAEQAVTIGPQSVAVARCV 175
 QY 150 AMASKPATTIRWPKG-NKELKGKSEVEEWSMDYTVTSQMLKVKHEDDGGVPVICOVEHFA 208
 DB 176 STGGRPPARITWISSLGGEAKOTQEPGIQAGTVTILSRYSLVPGVGRADGVKVCRCVEHES 235
 QY 209 VTGNLQORYLEVOYKPOVHIQNTYFLOGLTREGDAFELTCEALGKPOPMVMTWVRVDDE 268
 DB 236 FEPPIILLPVTLSVRYPEVSVIS--GYDDNMYLGRSEAI-LTCDVRSNPPEPTDYDMSTTSVG 293
 QY 269 MPQHAVLSGPNLFINNLTNDNGTYRCEASNIYVKAHSDYMLVYDPPPTTIPPTTTTTT 328
 DB 294 FPASAVAQSSQLLVHSDVRMNTFTCTAINAVGTGRAEQVILVRTPQA-----343
 QY 329 TTTTTLTITLITDSRAGEETIGADHVAIGGVAVVFA--MLCLLILGLRYFAHKG 386
 DB 344 -----SR-----DVGPLVWAGVGTTLLVLLAGFLAILLGRRRKSPG 384
 QY 387 TYPTHEAKGADDA-----ADADTAIINAEAGGONNSEEKKE 421
 DB 385 GGGNDGDRGSDPKPTQVFGNGGVFWRASAPPEMRPDGREDDEEEEEE 432

RESULT 5
 JC4024
 poliovirus receptor-related protein precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C:Accession: JC4024
 R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, C.; Dubre
 Gene 155, 261-265, 1995
 A:Title: Complementary DNA characterization and chromosomal localization of a human gene
 A:Reference number: JC4024; MUID:95237621; PMID:7721102
 A:Accession: JC4024
 A:Molecule type: mRNA
 A:Residues: 1-518 <LOP>
 A:Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
 C:Genetics:
 A:Gene: GDB:PVRR1
 A:Cross-references: GDB:583951
 A:Map position: 11q23-11q24
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 C:Keywords: glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F:356-379/Domain: transmembrane #status predicted <TM>
 F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.18; Score 244; DB 2; Length 518;
 Best Local Similarity 25.14%; Pred. No. 1e-09;
 Matches 104; Conservative 59; Mismatches 155; Indels 96; Gaps 20;

QY 56 IQLNPNRQTYFRDRLPKDSRFQNLNFSSELKSLTNVSISDGRYFCOLYTDPP-- 113
 DB 78 VAINPMSGVSLAPYR-----ERVEFLRPSFTDGTIRLSLELEDEGVYICEFATFTGN 133

QY 114 QBSYTTITVLVPPRNLMDIKD-TAVEGEIEV---NCTAMASKPATTIRWFKGNKEIK 169
 DB 134 RBSQLNLVMAKPTTWIEGTQAVLRKAKGQDDKVLVATCTTSANGKPPSVSW---ETRLK 190
 QY 170 GKSEV--EWSDM--YTVTSQMLKVKHEDDGGVPVICOVEHFAVTVGNLQORY-----LE 220
 DB 191 GEARVPGSGTPMAVTVISRYRLVPSREAHQOSLACIV-----NHYMDRFKSLTLN 243
 QY 221 VOYKPOVHIQ---MTYPLQGLTREGDAFELTCEALGKPOPMVMTWVRVDENPQHAVLSG 277
 DB 244 VOYEVEVTIEGFGWYLRQMD-----VKLTCKADANPATEYHHTTILNGSLPKGVEAQN 298
 QY 275 PNLFINN-LNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTIPPTTTTTTTTTT 336
 DB 299 RTLFFKGPINVLGTYICEATNPITGRSGQVEVNITFPYTPSP-----344
 QY 337 LTIIDSRAGEG-TIGAVDHAVIGGVAVVFA--MLCLLILGLRYFA-----RH--KGTYF 389
 DB 345 -----EHRRAGPVPTAIIGSVAGSI---LLVLIVGGI VVALRRRHTHFKGDYS 391
 QY 390 T-----HEAKGA-----DDAADADTAIINAEAGGONNSEEKKE 421
 DB 392 TKKHVYGVNGSKAGIPQHPHPMAQNLOYPDDSDDEKKA--GPLGGSSYEHEEE 443

RESULT 6
 A53437
 poliovirus receptor mpvr - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C:Accession: A53437
 R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
 J. Biol. Chem. 269, 8431-8438, 1994
 A:Title: Amino acid residues on human poliovirus receptor involved in interaction with
 A:Reference number: A53437; MUID:94179228; PMID:8132569
 A:Accession: A53437
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-530 <AOK>
 A:Cross-references: GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
 A:Experimental source: C57/BL6, brain
 A:Note: Sequence extracted from NCBI backbone (NCBI:146664, NCBI:146667)
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 11.1%; Score 243; DB 2; Length 530;
 Best Local Similarity 22.6%; Pred. No. 1-2e-09;
 Matches 90; Conservative 61; Mismatches 162; Indels 86; Gaps 14;

QY 4 PGLRLRLLLLSAALIPGTGQNLFTKDVTVIEGEV---ATISQV-----48
 DB 14 PTLPLPLLLLL---LQETG-AQDVVRVLPEVGRGLGTGTPCHLLPPTTVERVSQVT 68
 QY 49 -NKSDSVTQLNPNKQTYFRDRLPKDSRQL-----LNFSSSELKSLTNVSIS 99
 DB 69 WORLDGTVAFAHPS---FGVDFPNSQFSKORLSFVRARPETNADLRDATLAFRGLRVE 124
 QY 100 DGRYFCOLYTOP--POESVTTITVLVPRNLMIDIKQDAVEGEIEV-----NCT 149
 DB 125 DGNVTCFATPENGTRGVTWLRVIAQEN-----HAEQAVTIGPQSVAVARCV 175
 QY 150 AMASKPATTIRWPKG-NKELKGKSEVEEWSMDYTVTSQMLKVKHEDDGGVPVICOVEHFA 208
 DB 176 STGGRPPARITWISSLGGEAKOTQEPGIQAGTVTILSRYSLVPGVGRADGVKVCRCVEHES 235
 QY 209 VTGNLQORYLEVOYKPOVHIQNTYFLOGLTREGDAFELTCEALGKPOPMVMTWVRVDDE 268
 DB 236 FEPPIILLPVTLSVRYPEVSVIS--GYDDNMYLGRSEAI-LTCDVRSNPPEPTDYDMSTTSVG 293
 QY 269 MPQHAVLSGPNLFINNLTNDNGTYRCEASNIYVKAHSDYMLVYDPPPTTIPPTTTTTT 328
 DB 294 FPASAVAQSSQLLVHSDVRMNTFTCTAINAVGTGRAEQVILVRSPST-----343

A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <WIL>
A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone F15G9
R:Kershaw, J.
submitted to the EMBL Data Library, December 1994
A:Reference number: Z19929
A:Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5198 <W1>
A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A:Experimental source: clone T09B9
C:Genetics:
A:Gene: him-4; F15G9.4b
A:Map position: X
A:introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1

Query Match 11.9%; Score 261.5; DB 2; Length 5198;
Best Local Similarity 24.6%; Pred. No. 1.1e-09;
Matches 87; Conservative 65; Mismatches 130; Indels 71; Gaps 15;

QY 34 VTVIEGEVATISQVKNKSDSVIQLLNPNRQTIYRDFRPL----KDSRFOLLNFSSEL 89
DB 2200 VTAIKGGALPFCPID--DDK-----NFKQIILNRNQPIDLEAEDAKITRL---SNDR 2249
QY 50 KSVLTNVSIDEGRYFCQIYTPDPQESYT-TITVLVPPRLNLMIDIQK--TAVEGEEIEVN 147
DB 2250 RLTIILNVNDEQGYSCRVKNDAGENSPDKATVLVPPITIIIMLDKDKNTAVEHSTVLS 2309
QY 148 CTAMASKPATIITWPKG-----NKLKGKSEVEEWSDMYVTSQMLMKVHK 193
DB 2310 CPA-TGKPEPDITWFKDGBAIIENIADIIPGELNG-----NOLKITRIK 2354
QY 194 EDGQVPIQVEHPAVTGMLOQTVLEQVKQVH---IQMTYPLQGLTREGDAFELTCE 250
DB 2355 EGDAGKYTCEDNSA--GSVEQDVNVNVTIPKIEKDGIPSDYESQ---QNERVVISCP 2408
QY 251 AIGKPOPMVTVRVVDENPQHAVL-----SGPNLFINLNKNTDNGTYRCEASNIVGKAHS 306
DB 2409 VYARP-PAKITLWKAGKPLQSKFKVKTSAWGKQLVLFKLRETDSKYTCIATNEAGTKR 2467
QY 307 DMYLYVVDPTTIPP-----PTTITTTTTTTTTTITITITDSPACE 347
DB 2468 DFKVMVAPSDPEPNVIRITVNSGNPSTLHCPAKGSPSPITMLKOGNAIE 2520

RESULT 4
HLMSP3
poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
R:Accession: A38211
R:Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re-
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:47-133/Domain: immunoglobulin homolog <IMM1>
F:167-231/Domain: immunoglobulin homolog <IMM2>
F:267-322/Domain: immunoglobulin homolog <IMM3>
F:355-374/Domain: transmembrane #status predicted <TMN>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 12.283 Seconds

(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPPGLRLRLLLLLLSAAL.....TAINAEGGQNNSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	270	12.3	407	T08732	hypothetical prote
2	261.5	11.9	5175	T20992	hypothetical prote
3	261.5	11.9	5198	T43290	hemikenttin prote
4	246.5	11.2	467	HLMP3	poliovirus recepto
5	244	11.1	518	JC4024	poliovirus recepto
6	243	11.1	530	A53437	poliovirus recepto
7	238.5	10.9	538	T168093	poliovirus recepto
8	238	10.8	725	JEO099	neural cell adhesi
9	237	10.8	417	A44194	poliovirus recepto
10	234.5	10.7	392	B44194	poliovirus recepto
11	234	10.7	1088	IJXLNL	neural cell adhesi
12	232.5	10.6	392	1 RWHUPD	poliovirus recepto
13	232.5	10.6	417	1 RWHUPD	poliovirus recepto
14	231	10.5	344	I56551	neurotrophin - rat
15	228.5	10.4	7962	I38346	elastic titin - hu
16	226	10.3	4162	T42633	connectin/titin -
17	225	10.2	1011	T13669	neuroomusculin - fr
18	222	10.1	725	JE0100	neural cell adhesi
19	222	10.1	1092	1 JN0635	neural cell adhesi
20	220.5	10.0	338	JC5519	50K glycoprotein p
21	220	10.0	478	I53960	PRR2 alpha - human
22	217.5	9.9	345	S03199	opioid-binding pro
23	215.5	9.8	345	JC4025	opioid-binding cel
24	215.5	9.8	588	A45254	surface glycoprote
25	214	9.7	588	JH0506	adhesion molecule
26	212	9.6	4391	A38096	perlecan precursor
27	210.5	9.6	812	B42632	cell adhesion mole
28	210.5	9.6	932	A42632	cell adhesion mole
29	209.5	9.5	345	JC1239	opioid-binding pro

30	209.5	9.5	584	2	I50419	s-glycerin precurs
31	207.5	9.4	646	2	I38049	cell surface glyco
32	206.5	9.4	338	2	JC4776	limbic-system-asso
33	206.5	9.4	862	2	I49583	differentiation an
34	206.5	9.4	868	2	A4512	CD22 homolog/B lym
35	206	9.4	847	2	JH0371	B-cell adhesion pr
36	204	9.3	702	2	A36319	carcinoembryonic a
37	203.5	9.3	583	2	I39428	alcam - human
38	202	9.2	1443	2	I50600	neogenin - chicken
39	200.5	9.1	338	2	JC1238	opioid-binding pro
40	200.5	9.1	765	2	C42632	cell adhesion mole
41	200	9.1	587	2	JH0464	DM-GRASP precursor
42	197	9.0	3707	2	S18252	heparan sulfate pr
43	196.5	8.9	1241	2	T37190	nephlin - human
44	195	8.9	1323	2	PN0568	connectin 3B - chi
45	193	8.8	761	1	IJHUNG	neural cell adhesi

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKFP566B0846.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C;Accession: T08732

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16474

A;Accession: T08732

A;Molecule type: mRNA

A;Residues: 1-407 <OTT>

A;Cross-references: EMBL:AL050071

A;Experimental source: fetal kidney; clone DKFP566B0846

C;Genetics:

A;Note: DKFP566B0846.1

Query Match 12.3%; Score 270; DB 2; Length 407;

Best Local Similarity 27.0%; Pred. No. 11e-11;

Matches 85; Conservative 58; Mismatches 124; Indels 48; Gaps 13;

Qy	1C2	GRVFCOLYTD--PQESYTTITVLVPPRLMIDIQDXTAVEG--EIEVNCTAMASKPAT 157	
Db	2	GKTYCKAVTFPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDGNETVAAICIAATGKPA 60	
Qy	158	TIRWFKGNKELGKSEVEWSDMY-----TVTSQMLKVHKEDDGVVICQVHPAVTGN 212	
Db	61	HIDW-EGD-----LGEMESTTTSFNETATISQYKLFPTFRFARGRRITCVVXHPALEKD 114	
Qy	213	LOTQRYLEVQYKPVQHIQMTYPLQGLTREGDAPELTCFAIGKQPVMVTVVRVDEMPQH 272	
Db	115	IRYSFILDQYAPEVSVGTGVDGNWFGVRKG--VNLACNADANPPPKSVWSRLDGQWPDG 172	
Qy	273	AVLUSGNL-FINNINKDNGTYRCEASNIVGKAHSYMLVYVDP--TTIPP-----PTT 324	
Db	173	LLASDNLHFVHPLTENYSGVYICKVTNSIGQRSDQKVIYISDPPTTTTQPTIQWHPST 232	
Qy	325	TTTTTTTT-----TTTLTITITSRAGEECTIGAVDHAIVIGGVAVVVFAMLCILI- 375	
Db	233	ADIEDLATPKLPPFLPLTLATI-----KODTIATIIASVVGVALFVLVSLAGIFC 285	
Qy	376	-----ILGRYFARH 384	
Db	286	YRERRTRFGDYFAKN 300	

RESULT 2

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20992; T24733

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QY      279  TWVRVDDWMPQHAVLUSGPNLFNNIKNDNTGYCEASNIUGKAHSYMLVYVDDPPTTP 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      300  LWEK-EGSVPLPKMTQESALIFPFLNKSDSGTGYCTATSNMGSKAYVITLNVNDPS---P 355
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      339  PPTTITTTTTTTTTTTTTILITIDSRAGEBSIRAVDHVIGSVAVVVFAMLCILIIIGRY 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      356  VPSSSTY-----HAIGGIIVAFIVFLIIIMLIFLGHY 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      399  FARHGKTYTFTHKAGDADAADATTAIINAEQGQNNSEKKEYFI 442
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      389  LIIRHKGTYLTHEAKGSDDAPADTAIINAEQGQSGDDKKEYFI 432
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373

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```
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mathier, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902/775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

Qy 22 PGLRLRLRLFLSAAALPTG-----DQNLFTKDVTVIEGEVATISCOVKNKSDSVIQL 76
Db 4 PAASLLLLLLLF-ACCWAPGGANLSQDQSQWTSDETVAAGTVLKKQVKKDHEDSSLOW 62
Qy 77 LNPNRQTIYFRDPLKDSRFLQNLNFSSELKSLVNTSVISDEGRYFCQLYTDPPEQSYT 136
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Db 63 SNPAQQTLYFGEKRALRDNRIQLVSTPHELSSISNVALADEGEYTCSTFTMPVRTAKS 122
Qy 137 TITVLVPPRLNLMIDIOKDTAVEGEEIEVNCVTAMASKPATIRWFKGNTELKKG-SEVEEW 195
Db 123 LVTVLGIPQPIITGYKSSREKDTATINCQSGSKPAARLTWRKQGEUHGEPRIQED 182
Qy 196 SD--MYTTSQLMLKVHKEDDGVFVQCQVHPAVTG-NLQOTRYLEYQYKPVQHIQMTYP 252
Db 183 PNGKTFVSSSVTFQVTRDEDDGASIVCSVNHESLKGAADRSTSQRIEVLVYPTAMIRDPDP 242
Qy 253 LQGLTREGDALEITCEAIGKQPQVWTVWVRVDEMPQHAVLSGPNLFINNLTNDGTYR 312
Db 243 ---HPRREGQKLLHCEGRGNPVFQYLWER-EGSVPLPKMTQESALIFPFLINKSDSGTYG 298
Qy 313 CEASNIVGKAHSDYMLVYDPPPTTIPPTTTTITTTTTTTTTTTTTTTTTITITDSRAGEBSIRAV 372
Db 299 CTATSNMGSKAYTLNVNDFS---PVPSSSSYV----- 329
Qy 373 DHAIVGGVAVVVPFAMCLLIILGRYPARHKGYTTFHEAKGADDAADADTAIINAEGGON 432
Db 330 -HAIGGIVAFIVFLLIIMLIFLGHVLRHKGYTLTHEAKGSDDAPADTAIINAEGGQS 388
Qy 433 NSEKKEYFI 442
Db 389 GGDDKKEYFI 398

RESULT 14
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match      31.6%; Score 722; DB 4; Length 432;
Best Local Similarity 36.4%; Pred. No. 4.9e-55;
Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;

Qy 22 PGLRLRLRLFLSAAALPTG-----DQNLFTKDVTVIEGEVATISCOVKNKSDSVIQL 47
Db 4 PAASLLLLLLLF-ACCWAPGGANLSQDQSQWTSDETVAAGTVLKKQVKKDHEDSSLOW 62
Qy 48 -----FTKDVTVIEGEVATISCOVKNKSDSVIQLNPNRQTIYFRDPLKDSRFLQNL 102
Db 63 QDSQWTSDETVAAGTVLKKQVKKDHEDSSLOWNSAQOTLYFGEKEALRDNRIQLVTS 122
Qy 103 SSSELKSLVNTSVISDEGRYFCQLYTDPPEQSYTITVLVPPRLNLMIDIOKDTAVEGEEI 162
Db 123 TPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTLGIPQPIITGYKSSLRKDTA 182
Qy 163 EVNCTAMASKPATIRWFKGNTELKKG-SEVEWSD--MYTTSQLMLKVHKEDDGPVVI 219
Db 183 TLNCQSGSKPAARLTWRKQGEUHGEPRIQEDNKFTVSSSVTFQVTRDEDDGASIV 242
Qy 220 COVEHPAVTG-NLQOTRYLEYQYKPVQHIQMTYFLOGLTREGDALEITCEAIGKQPQVW 278
Db 243 CSVNHESLKGAADRSTSQRIEVLVYPTAMIRDPDP---HPREGQKLLHCEGRGNPVFPQY 299
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; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-778-510-6

Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

Qy 22 PGLRLRLRLLLFSAALIPGT-----DQNLFTKDVTVIEGEVATISQVKNKSDSVIQL 76
Db 4 PAASLLRLRLLLF-ACCWAPGGANLSQDSDSQPWTSDETVAGTVVLKQVKDHEDSSLQW 62

Qy 77 LNPNQTIYFRDFRPLKDSRFQLNFSSELKVSILTNVSIISDEGRYFCQLYTDPQESYT 136
Db 63 SNPAQOTLYFGEKRALDRNRQLVTSITPHELSISISNVALADGEYTCISFTMPVRTAKS 122

Qy 137 TITVLVPPRNLMDIQKDTAVEGEEIEVNCAMASKPATTIRWFKGNTELKKG-SEVEEW 195
Db 123 LVTVLGIPQKIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKQDELHGEPTRIQED 182

Qy 196 SD--MYTVTSQMLKVHEDDGVVICQVEHPAVTG-NLQTRYLEVQYKQVHIQMTYP 252
Db 183 PNGKTFVTSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRILEVLYTPTMIRPDPP 242

Qy 253 LQGLTRGDALCEATGKQPQVWVWVVRVDDDEMPQHAVLSGNLFINNLKNTDNGTYR 312
Db 243 ---HPREQKULLHCEGNGVNPQOYLWEK-EGSVPLPKMTQESALIPFLNKLSDSGTYG 298

Qy 313 CEASNIVGKAHSDVYLYVDPPTTIPPTTTTPTTTTPTTTTITITITDSRAGEGSIKAV 372
Db 299 CTATSNMGSYKAYTLNVNDS---PVSSSTY----- 329

Qy 373 DHAIVGGVAVVVFAMLCILLIIRYFARHKGTYFTHEAKGADDAADADTAIINAEQQN 432
Db 330 -HAIGGIVAFIVFILLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAEQQS 388

Qy 433 NSEKKEYFI 442
Db 389 GGDKKEYFI 398

RESULT 11
US-09-778-794A-84
; Sequence 84, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-907-794A-84

Query Match 32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.4e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps 9;

Qy 22 PGLRLRLRLLLFSAALIPGT-----DQNLFTKDVTVIEGEVATISQVKNKSDSVIQL 76
Db 4 PAASLLRLRLLLF-ACCWAPGGANLSQDSDSQPWTSDETVAGTVVLKQVKDHEDSSLQW 62

Qy 77 LNPNQTIYFRDFRPLKDSRFQLNFSSELKVSILTNVSIISDEGRYFCQLYTDPQESYT 136
Db 63 SNPAQOTLYFGEKRALDRNRQLVTSITPHELSISISNVALADGEYTCISFTMPVRTAKS 122

Qy 137 TITVLVPPRNLMDIQKDTAVEGEEIEVNCAMASKPATTIRWFKGNTELKKG-SEVEEW 195
Db 123 LVTVLGIPQKIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKQDELHGEPTRIQED 182
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Db 363 VVFTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEGSQVNAEKKKEYFI 421

RESULT 8

US-08-660-531-1

; Sequence 1, Application US/08660531

; Patent No. 6221845

; GENERAL INFORMATION:

; APPLICANT: Chrysler, Susanna M.S.

; APPLICANT: Sinha, Sukanto

; APPLICANT: Keim, Pamela S.

; APPLICANT: Anderson, John P.

; TITLE OF INVENTION: Beta-Secretase

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Ctr., 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,531

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/480,498

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15270-002210US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 421 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-660-531-1

Query Match 39.2%; Score 895.5; DB 3; Length 421;

Best Local Similarity 45.1%; Pred. No. 2.9e-70;

Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 44 GQLFTKDVTVIEGAVATISQVKNKSDSVTLQNLNPNRTIYFDRPLKDSRFQLNFS 103

Db 10 GQPLTONVTVIEGTAILECRVDQNTSLQSNPAQQTLYFDKALRDNRIELVRAS 69

QY 104 SSELKVSILTUNVISDEGRYFCOLYDPPQESYTTITVLVPPRNLMIDIQDVAEGEEIE 163

Db 70 WHELSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSPVMEGLMQ 129

QY 164 VNCETAMASKATTIRWPKGNTELKGEVEBWS---DMYVTSQMLKVKHKDDGVVVIC 220

Db 130 LTCKTSGSKPAADIRWFKNDKEIKDVLYLKEEDANRKTFTVSSLDVFRDSDGVAVIC 189

QY 221 QVEHPAVTGNLQ-TQRYLEVQYKQVHIQMTYPLQGLTRGDALCEALGKQPVMVT 279

Db 190 RVDESINATPQAVAMQVLEIHTYTSVKI---IPSTPPQEQPLILICESKGPLPEPVL 246

QY 280 WVRVDDM--PQHAVLSGPNLFINNKNKTNGTYRCEASNIYVKAHSDYMLYVYDPPPTTI 337

Db 247 WTKDGGELPDPDRMVWSGREINILFNKNTDNGTYRCEATNTIGQSSAEYVLIVHDVNTL 306

QY 338 PPPTTTTTTTTTTTTTTTTTTTTT-----DSRAGEEGSIRAVDHAIVGGVVAV 383

Db 307 LPTTIIPSLTATVTTVAITTSPTTSATTSIRDPNALAQNGP----DHALLGGIVAV 362

QY 384 VVFAMLCILLIILGRYFARHKGTYFTHKAGDAADADTAIINAEGSQVNAEKKKEYFI 442

Db 363 VVFTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEGSQVNAEKKKEYFI 421

RESULT 9

US-09-778-510-4

; Sequence 4, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; TITLE OF INVENTION: Molecules Designated B7L1

; FILE REFERENCE: 2844-US

; CURRENT APPLICATION NUMBER: US/09/778,510

; CURRENT FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: PCT/US99/17906

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/095,663

; PRIOR FILING DATE: 1998-08-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 398

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-778-510-4

Query Match 32.7%; Score 745.5; DB 4; Length 398;

Best Local Similarity 39.1%; Pred. No. 3.7e-57;

Matches 172; Conservative 74; Mismatches 137; Indels 57; Gaps 11;

QY 16 AAAAAPELLRLRLLLLLFSAAALIPGT-----DQNLFTKDVTVIEGAVATISQVKNKSD 70

Db 3 APAASP-----VPLLLLL--ACSWAPGGANLSQDSDSQPWTSDETVWAGTVVLKQVKDHE 56

QY 71 DSVIQLLNPNRTIYFDRPLKDSRFQLNFSSELKVSILTUNVISDEGRYFCOLYDTP 130

Db 57 DSSLQSNPAQQTLYFGEKALRDNRIQLVSSITPHELISISINVALADEGEYTCISITMP 116

QY 131 PQESYTTITVLVPPRNLMIDIQDVAEGEEIEVNCETAMASKPATIRWPKGNTELKQ-K 189

Db 117 VRTAKSLVTVLGIPIQKPIITGYKSSLREKETATLNCQSSGSKPAQAQLTWKGDQELHGDQ 176

QY 190 SEVEEWSK--MYTVTSQMLKVKHKDDGVPIQVEHPAVTG-NLQTRYLEVQYKQVH 246

Db 177 TRIQEDPNGKTFVSSSVSPQVTRDDGANIVGSVNHESLKGADRSQSRIEVLVYTPETAM 236

QY 247 IQMTYPLQGLTRGDALCEALGKQPVMVTWVRVDDMPP---QHAVLSGPNLFINN 302

Db 237 IR---PEPAHPREGQKLLHCEGNGPVPQOYVWVKEGSEPPPLKMTQESALIFP----F 288

QY 303 LNKTDNGTYRCEASNIYVKAHSDYMLYVYDPPPTTIPTTTTTTTTTTTTTTTTTTTTTIITDSR 362

Db 289 LNKSDSGTYCTATSNMGSYTAFTLNVNDPS---PVPSSSTV----- 329

QY 363 AGEESIRAVDHAIVGGVAVVFPAMCLLIILGRFARHKGTYFTHKAGDAADADT 422

Db 330 -----HAIIGGIVAFIVFLLILLIFLGHYLIIRHKGYLTLEAKGSDADPADT 378

QY 423 AIINAEGSQVNAEKKKEYFI 442

Db 379 AIINAEGSQSGGDDKKEYFI 398

RESULT 10

US-09-778-510-6

; Sequence 6, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:


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; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: prt
; ORGANISM: Mus musculus
US-09-778-510-22

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Query Match	95.0%,	Score	2169,	DB	4;	Length	423;
Best Local Similarity	98.8%;	Pred.	No. 6.1e-162;				
Matches	418;	Conservative	1;	Mismatches	4;	Indels	0;
Gaps	0;						

QY	19	AAPPGRLRLRLLLLSAAALIP	TG	GGQNLFTK	QV	TVIEGEVATIS	CQV	NKSDSDSVIQLLN	78	
DB	1	AAPPGLERLRLLLLSAAALIP	TG	GGQNLFTK	QV	TVIEGEVATIS	CQV	NKSDSDSVIQLLN	60	
QY	79	PNRQTIYFRDPRPLKDSRFQ	LLN	PSSELKVS	LN	INVSISDEGR	YFCQ	LYTDPPOESYTTI	138	
DB	61	PNRQTIYFRDPRPLKDSRFQ	LLN	PSSELKVS	LN	INVSISDEGR	YFCQ	LYTDPPOESYTTI	120	
QY	139	TVLVPPPNLMDIQKDTAVE	GEELV	EVNCTAM	ASKPAT	TI	RWFKNG	NTELK	KGKSEVEE	198
DB	121	TVLVPPPNLMDIQKDTAVE	GEELV	EVNCTAM	ASKPAT	TI	RWFKNG	NTELK	KGKSEVEE	180
QY	199	YTVTSQMLKVHKHEDDGP	VI	CQVEH	PAV	TGN	LOTQRY	LEVQY	KPQVHI	258
DB	181	YTVTSQMLKVHKHEDDGP	VI	CQVEH	PAV	TGN	LOTQRY	LEVQY	KPQVHI	240
QY	259	EGDALELTCEAIGKQPQ	PV	MTW	RV	DD	EMPO	HAVL	SGNLF	318
DB	241	EGDAFELTCEAIGKQPQ	PV	MTW	RV	DD	EMPO	HAVL	SGNLF	300
QY	319	VGAHSDYMLYVDDPPT	TI	PP	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTT	TT	TSR	378
DB	301	VGAHSDYMLYVDDPPT	TI	PP	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTT	TT	TSR	360
QY	379	GVAVVVVFMCLLLII	IG	RYFAR	HKG	YTF	THE	AKG	ADDA	438
DB	361	GVAVVVVFMCLLLII	IG	RYFAR	HKG	YTF	THE	AKG	ADDA	420
QY	439	EYF	441							
DB	421	EYF	423							

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RESULT 5
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten
; TITLE OF INVENTION: Assays for Detection of Infection
; TITLE OF INVENTION: Inhibition of Infection
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend
; STREET: Two Embarcadero Ctr.,
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.

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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/659,984A
? FILING DATE: 07-JUN-1996
? CLASSIFICATION: 436
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/485,152
? FILING DATE: 07-JUN-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Heslin, James M.
? REGISTRATION NUMBER: 29,541
? REFERENCE/DOCKET NUMBER: 15270-00281005
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-326-2400
? TELEFAX: 415-326-2422
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 444 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-659-984A-5

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Query Match.	39.5%;	Score 902;	DB 2;	Length 444;
Best Local Similarity	44.6%;	Pred. No. 8.3e-71;		
Matches 194;	Conservative	74;	Mismatches 137;	Indels 30; Gaps 7

QY	31	LLFSAAA--LIP	TGDCGNLF	TKDVT	VEGRVAT	IS	COVNKSD	SDSV	LI	LNPN	RCTI	YF	87
DB	17	LLLQAAAK	NKVKVGS	QCOF	PLTQ	NVT	VEGGT	ALT	CRVD	QDN	TSL	OWNS	PAO
QY	88	DFRPLK	DSRFQ	LLNF	SSSEL	KVSL	TNYS	I	SD	EGY	FQ	LY	TD
DB	77	DKKAL	RNR	IEL	VRAS	WHELS	IS	VS	D	SL	SD	EGY	TS
QY	148	MIDIQ	KD	TA	VE	GE	BE	I	EVN	C	TAM	ASK	P
DB	137	QISGF	SPV	ME	GL	MQ	LT	CT	SG	S	K	P	A
QY	205	LMK	VKH	KD	GV	PV	I	CV	Q	VE	H	PA	T
DB	197	LDFR	V	DR	S	D	GV	A	V	I	CR	V	D
QY	264	EL	CE	A	I	G	K	P	Q	P	V	M	T
DB	254	IL	T	C	S	G	K	E	L	P	P	V	L
QY	322	AH	S	D	Y	M	L	V	D	P	P	T	T
DB	314	SSA	E	Y	L	V	H	D	V	E	N	T	L
QY	368	SIR	A	V	H	A	V	I	G	V	V	V	F
DB	374	P----	D	H	A	L	I	G	G	I	V	A	V
QY	428	E	G	Q	N	N	S	E	E	K	E	Y	F
DB	430	E	G	S	O	V	N	A	E	E	K	E	Y

RESULT 6
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP

Qy 361 SRAGEGSIKRAVDHAGVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEGSIKRAVDHAGVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Qy 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 2

US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JH01770-1
; CURRENT APPLICATION NUMBER: US/09/930.803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 100.0%; Score 2283; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 6.6e-192;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDQNLFTKDVTVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDQNLFTKDVTVIEGEVA 60
Qy 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILTVNSISDEG 120
Db 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILTVNSISDEG 120
Qy 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDQTAVEGEEIEVNCNTAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDQTAVEGEEIEVNCNTAMASKPATIRWF 180
Qy 181 KGNTLKGKSEVESEWSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVESEWSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 240
Qy 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFI 300
Qy 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTITD 360
Qy 361 SRAGEGSIKRAVDHAGVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 361 SRAGEGSIKRAVDHAGVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Qy 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 3

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866.028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-866-028-61

Query Match 99.1%; Score 2263; DB 4; Length 440;
Best Local Similarity 99.5%; Pred. No. 3.7e-190;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDQNLFTKDVTVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDQNLFTKDVTVIEGEVA 58
Qy 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILTVNSISDEG 120
Db 59 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKVSILTVNSISDEG 118
Qy 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDQTAVEGEEIEVNCNTAMASKPATIRWF 180
Db 119 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDQTAVEGEEIEVNCNTAMASKPATIRWF 178
Qy 181 KGNTLKGKSEVESEWSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 240
Db 179 KGNTLKGKSEVESEWSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLQORYLEVQ 238
Qy 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFI 300
Db 239 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFI 298
Qy 301 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTITD 360
Db 299 NNLKNTDNGTYRCEASNIUGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTITD 358
Qy 361 SRAGEGSIKRAVDHAGVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 359 SRAGEGSIKRAVDHAGVIGGVVAVVVFAMLCIIILGRYFARHKGTYFTHEAKGADDAADA 418
Qy 421 DTAINAEGGQNNSEKKEYFI 442
Db 419 DTAINAEGGQNNSEKKEYFI 440

RESULT 4

US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 8512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778.510

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 16.1676 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-2

Perfect score: 2283
Sequence: 1 MASVLPSSGSCAAAAA.....AIINREGQNNSEKKEYFI 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2283	100.0	442	4	US-09-778-510-20
2	2283	100.0	442	4	US-09-930-803-1
3	2263	99.1	440	4	US-09-866-028-61
4	2169	95.0	423	4	US-09-778-510-22
5	902	39.5	444	2	US-08-659-984A-5
6	902	39.5	444	3	US-08-660-531-5
7	895.5	39.2	421	2	US-08-659-984A-1
8	895.5	39.2	421	3	US-08-660-531-1
9	745.5	32.7	398	4	US-09-778-510-4
10	739	32.4	398	4	US-09-778-510-6
11	739	32.4	398	4	US-09-907-794A-84
12	739	32.4	398	4	US-09-905-125A-84
13	739	32.4	398	4	US-09-902-775A-84
14	722	31.6	432	4	US-09-778-510-2
15	335	14.7	227	4	US-09-205-258-947
16	256.5	11.2	517	4	US-09-723-368-4
17	248	10.9	518	4	US-09-919-172-20
18	232	10.2	393	1	US-08-439-742-2
19	226	9.9	479	4	US-09-723-368-2
20	222	9.7	458	4	US-09-435-956A-1
21	220.5	9.7	344	4	US-09-700-397-3
22	211	9.2	313	4	US-08-700-397-4
23	208	9.1	388	1	US-08-429-742-4
24	206	9.0	642	1	US-08-217-299-1
25	206	9.0	698	2	US-08-602-725-36
26	206	9.0	734	2	US-08-389-459A-17
27	206	9.0	734	3	US-08-987-867A-17

28	205.5	9.0	338	4	US-09-976-594-404	Sequence 404, App
29	205.5	9.0	1461	4	US-09-976-594-531	Sequence 531, App
30	200.5	8.8	308	2	US-08-414-657D-46	Sequence 46, Appl
31	200.5	8.8	325	2	US-08-414-657D-2	Sequence 2, Appl
32	200.5	8.8	325	2	US-08-414-657D-41	Sequence 41, Appl
33	200.5	8.8	325	2	US-09-135-080-2	Sequence 2, Appl
34	199.5	8.7	338	2	US-08-414-657D-42	Sequence 42, Appl
35	199.5	8.7	338	2	US-08-414-657D-43	Sequence 43, Appl
36	199.5	8.7	338	2	US-09-135-080-4	Sequence 4, Appl
37	199.5	8.7	1241	3	US-09-040-774-2	Sequence 2, Appl
38	199	8.7	582	4	US-09-702-705-334	Sequence 334, App
39	199	8.7	582	4	US-09-736-457-334	Sequence 334, App
40	199	8.7	582	4	US-09-614-124B-334	Sequence 334, App
41	199	8.7	582	4	US-09-671-325-334	Sequence 334, App
42	199	8.7	582	4	US-09-589-184-334	Sequence 334, App
43	198.5	8.7	315	2	US-08-414-657D-47	Sequence 47, Appl
44	198.5	8.7	408	4	US-09-724-864-62	Sequence 62, Appl
45	197.5	8.7	338	2	US-08-414-657D-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B711
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

Query Match					100.0%; Score 2283; DB 4; Length 442;
Best Local Similarity					100.0%; Pred. No. 6.6e-192;
Matches					442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	61	TISCQVNSDDSYIQLNPNRQTYFRDPLKDSFOLLNFS	120		Sequence 4, Appl
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Db	121	RYFCOLYTDPPQPSYTTITVLVPPNLMIDIQKDTAVE	180		Sequence 84, Appl
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Db	181	KGNTLKGKSEBWSDMYVTVSQMLKVHKKDDGVPIQ	240		Sequence 1, Appl
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Db	241	YKQVHIQMTYPIQGLTREGDALELCEAIKQCPVMV	300		Sequence 4, Appl
Qy	301	NNLKTNDGTYRCEASNIQVKAHSDYMLYVDPPTT	360		Sequence 17, Appl
Db	301	NNLKTNDGTYRCEASNIQVKAHSDYMLYVDPPTT	360		Sequence 17, Appl

Best Local Similarity 99.5%; Pred. No. 3.4e-175;			
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
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Db	1	MASVVLPSGSQCAAAAAAAPPGLRLRLLLLSAAALIP	58
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Db	119	RYFCQLYTDPPQESYTTITVLVPPRNLMIDIKOTAVE	178
Qy	181	KGNTLKGKSEVEEWSDMYTVTSQLMLKVHKEDDGPV	240
Db	179	KGNTLKGKSEVEEWSDMYTVTSQLMLKVHKEDDGPV	238
Qy	241	YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPVM	300
Db	239	YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPVM	298
Qy	301	NNLNKTDNGTYRCEASNIVGKAHSDYMLVYDPPPT	360
Db	299	NNLNKTDNGTYRCEASNIVGKAHSDYMLVYDPPPT	358
Qy	361	SRAGEGSIRAVDHAVIGGVAVVVFAMLCLLIILGRY	420
Db	359	SRAGEGSIRAVDHAVIGGVAVVVFAMLCLLIILGRY	418
Qy	421	DTAIINAEQQNNSEEKEYFI	442
Db	419	DTAIINAEQQNNSEEKEYFI	440

Search completed: May 27, 2004, 09:52:20
Job time : 39.5504 secs

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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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Db 1 MASVLPSSGSCAAAAAAPPGL--LRLLLLFSAAALPTGDCGNLFTKDVTVIEGEVA 58
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Db 59 TISQVKNKSDSVIQLLNPQRQTIYFRDPLKDSRFOLLNFSSELKVSILTNVISDEG 118
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Db 179 KGNTLKGKSEVEWSDMYTTSOLMLKVHEDDGVVICOVEHPAVTGNLQORYLEVQ 238
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Db 299 NNLKNTDNGTVRCASNIIVGAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTITD 358
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Db 359 SRAGEEGSIRAVDHAVIGGVVVVVFAMLCLLIILGRYFARHKQTYTFHEAKGADDAADA 418
Qy 421 DTAIINAGGQNNSEKKEYPI 442
Db 419 DTAIINAGGQNNSEKKEYPI 440

RESULT 15
US-09-945-015-61
; Sequence 61, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,015
; CURRENT FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
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; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,596
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-015-61
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Query Match

99.1%; Score 2263; DB 9; Length 440;

Best Local Similarity 99.5%; Pred. No. 3.4e-175; Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
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Db	1	MASVVLPSGSCAAAAAAPPGLRLRLLLLSAALIPGTGQGNLFTKDVTVIEGVA	58
QY	61	TISCQVNSDSDSVIQLLNPNRQTIYFRDRPLKDSRFOLLFSSSELKVSILTNVSIISDEG	120
Db	59	TISCQVNSDSDSVIQLLNPNRQTIYFRDRPLKDSRFOLLFSSSELKVSILTNVSIISDEG	118
QY	121	RYFCOLYTDPPQESYTTITVLVPPRNLMDIQKOTAVEGEIEVNCNTAMAKPATIRWF	180
Db	119	RYFCOLYTDPPQESYTTITVLVPPRNLMDIQKOTAVEGEIEVNCNTAMAKPATIRWF	178
QY	181	KGNTLKGKSEVEEWSMDYTVTSQMLKVKHEDDGVVICQVEHPAVTGNLQTOYRILEVQ	240
Db	179	KGNTLKGKSEVEEWSMDYTVTSQMLKVKHEDDGVVICQVEHPAVTGNLQTOYRILEVQ	238
QY	241	YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVVMVTVVRVDDMPQHAVLSPNLF	300
Db	239	YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVVMVTVVRVDDMPQHAVLSPNLF	298
QY	301	NLANKDNGTVRCASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTITD	360
Db	299	NLANKDNGTVRCASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTITD	358
QY	361	SRAGEGSIRAVDHAVIGSVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA	420
Db	359	SRAGEGSIRAVDHAVIGSVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA	418
QY	421	DTAINAEGGQNNSEKKEYFI 442	
Db	419	DTAINAEGGQNNSEKKEYFI 440	
RESULT 14			
US-09-945-587-61			
; Sequence 61, Application US/09945587			
; Patent No. US20020127643A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin			
; APPLICANT: Borstein, David			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Geritsen, Mary			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul			
; APPLICANT: Grimaldi, Christopher			
; APPLICANT: Gurney, Austin			
; APPLICANT: Hillan, Kenneth			
; APPLICANT: KJavin, Ivar			
; APPLICANT: Napier, Mary			
; APPLICANT: Roy, Margaret			
; APPLICANT: Thomas, Daniel			
; APPLICANT: Wood, William			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P2548P1C1			
; CURRENT APPLICATION NUMBER: US/09/945,587			
; CURRENT FILING DATE: 2001-09-26			
; PRIOR APPLICATION NUMBER: 09/866,028			
; PRIOR FILING DATE: 2001-05-25			
; PRIOR APPLICATION NUMBER: 60/067,411			
; PRIOR FILING DATE: December 3, 1997			
; PRIOR APPLICATION NUMBER: 60/069,334			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,335			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,278			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,425			

;	PRIOR FILING DATE: December 12, 1997
;	PRIOR APPLICATION NUMBER: 60/069,696
;	PRIOR FILING DATE: December 16, 1997
;	PRIOR APPLICATION NUMBER: 60/069,694
;	PRIOR FILING DATE: December 16, 1997
;	PRIOR APPLICATION NUMBER: 60/069,702
;	PRIOR FILING DATE: December 16, 1997
;	PRIOR APPLICATION NUMBER: 60/069,870
;	PRIOR FILING DATE: December 17, 1997
;	PRIOR APPLICATION NUMBER: 60/069,873
;	PRIOR FILING DATE: December 17, 1997
;	PRIOR APPLICATION NUMBER: 60/068,017
;	PRIOR FILING DATE: December 18, 1997
;	PRIOR APPLICATION NUMBER: 60/070,440
;	PRIOR FILING DATE: January 5, 1998
;	PRIOR APPLICATION NUMBER: 60/074,086
;	PRIOR FILING DATE: February 9, 1998
;	PRIOR APPLICATION NUMBER: 60/074,092
;	PRIOR FILING DATE: February 9, 1998
;	PRIOR APPLICATION NUMBER: 60/075,945
;	PRIOR FILING DATE: February 25, 1998
;	PRIOR APPLICATION NUMBER: 60/112,850
;	PRIOR FILING DATE: December 16, 1998
;	PRIOR APPLICATION NUMBER: 60/113,296
;	PRIOR FILING DATE: December 22, 1998
;	PRIOR APPLICATION NUMBER: 60/146,222
;	PRIOR FILING DATE: July 28, 1999
;	PRIOR APPLICATION NUMBER: PCT/US98/19330
;	PRIOR FILING DATE: September 16, 1998
;	PRIOR APPLICATION NUMBER: PCT/US98/25108
;	PRIOR FILING DATE: December 1, 1998
;	PRIOR APPLICATION NUMBER: 09/216,021
;	PRIOR FILING DATE: December 16, 1998
;	PRIOR APPLICATION NUMBER: 09/218,517
;	PRIOR FILING DATE: December 22, 1998
;	PRIOR APPLICATION NUMBER: 09/254,311
;	PRIOR FILING DATE: March 3, 1999
;	PRIOR APPLICATION NUMBER: PCT/US99/12252
;	PRIOR FILING DATE: June 22, 1999
;	PRIOR APPLICATION NUMBER: PCT/US99/21090
;	PRIOR FILING DATE: September 15, 1999
;	PRIOR APPLICATION NUMBER: PCT/US99/28409
;	PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;	PRIOR APPLICATION NUMBER: PCT/US99/28313
;	PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
;	PRIOR APPLICATION NUMBER: PCT/US99/28301
;	PRIOR FILING DATE: December 1, 1999
;	PRIOR APPLICATION NUMBER: PCT/US99/30095
;	PRIOR FILING DATE: December 16, 1999
;	PRIOR APPLICATION NUMBER: PCT/US00/03565
;	PRIOR FILING DATE: February 11, 2000
;	PRIOR APPLICATION NUMBER: PCT/US00/04414
;	PRIOR FILING DATE: February 22, 2000
;	PRIOR APPLICATION NUMBER: PCT/US00/05841
;	PRIOR FILING DATE: March 2, 2000
;	PRIOR APPLICATION NUMBER: PCT/US00/08439
;	PRIOR FILING DATE: March 30, 2000
;	PRIOR APPLICATION NUMBER: PCT/US00/14042
;	PRIOR FILING DATE: May 22, 2000
;	PRIOR APPLICATION NUMBER: PCT/US00/20710
;	PRIOR FILING DATE: July 28, 2000
;	PRIOR APPLICATION NUMBER: PCT/US00/32678
;	PRIOR FILING DATE: December 1, 2000
;	PRIOR APPLICATION NUMBER: PCT/US01/06520
;	PRIOR FILING DATE: February 28, 2001
;	NUMBER OF SEQ ID NOS: 120
;	SEQ ID NO 61
;	LENGTH: 440
;	TYPE: PRT
;	ORGANISM: Homo Sapien
;	US-09-945-587-61

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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDGNLFKDVTVIEGVA 60
DB 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPFGDGNLFKDVTVIEGVA 58
QY 61 TISQVKNKSDSVIQLLNPQRQTIYFRDRLKDSRFOLLNPFSSSELKVSILNVSISDEG 120
DB 59 TISQVKNKSDSVIQLLNPQRQTIYFRDRLKDSRFOLLNPFSSSELKVSILNVSISDEG 118
QY 121 RYFQCLYTDPPQESYTTTIVLVPBNLMIDIKOTAVEGSEIEVNCETAMASKPATIRWF 180
DB 119 RYFQCLYTDPPQESYTTTIVLVPBNLMIDIKOTAVEGSEIEVNCETAMASKPATIRWF 178
QY 181 KGNTELKGSVEEWSDMYTVTSQMLKVKHEDDGVVICQVEHPAVTGNLQTOXYLEVQ 240
DB 179 KGNTELKGSVEEWSDMYTVTSQMLKVKHEDDGVVICQVEHPAVTGNLQTOXYLEVQ 238
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTWVRVDDMPQHAVLSGPNLFI 300
DB 239 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTWVRVDDMPQHAVLSGPNLFI 298
QY 301 NNLKNTDNGTYRCASNIYVGVVAVVVFVAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
DB 299 NNLKNTDNGTYRCASNIYVGVVAVVVFVAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
QY 421 DTAINAEGGQNNSEKKEYFI 442
DB 419 DTAINAEGGQNNSEKKEYFI 440

RESULT 13
US-09-944-862-61
; Sequence 61, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,862
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-862-61

Query Match 99.1%; Score 2263; DB 9; Length 440;
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Best Local Similarity 99.5%; Pred. No. 3.4e-175;			
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;			
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Db	1	MASVVLPSGSCAAAAAAPPGLRLRLLLIFSAALIPGTGDNLFKDVTVIEGVA	58
QY	61	TISQVNSDSDSVIQLLNPRTIYFRDPRPLKDSRFQLLNFSSELKVSNTNVSISDEG	120
Db	59	TISQVNSDSDSVIQLLNPRTIYFRDPRPLKDSRFQLLNFSSELKVSNTNVSISDEG	118
QY	121	RYFCOLYTDPPQESTYTTIVLPPRENLMIDQKPAVEGEIEVNCNTAMAKPATIRWF	180
Db	119	RYFCOLYTDPPQESTYTTIVLPPRENLMIDQKPAVEGEIEVNCNTAMAKPATIRWF	178
QY	181	KGNTLKGKSEVEWSDMYTTSQMLKVKHEDDGVVICQVEHPAVTGNLQTKORYLEVO	240
Db	179	KGNTLKGKSEVEWSDMYTTSQMLKVKHEDDGVVICQVEHPAVTGNLQTKORYLEVO	238
QY	241	YKQVHIOMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSPNLF	300
Db	239	YKQVHIOMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDMPQHAVLSPNLF	298
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Db	299	NNLKNKTNGTYRCASNIYVGAHSDYMLVYVDPPTIIPPTTTTTTTTTTTTTTTTT	358
QY	361	SRAGEGSIRAVDHAVIGGVVAVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADA	420
Db	359	SRAGEGSIRAVDHAVIGGVVAVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADA	418
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Db	419	DTALINAGGQNNSEKKEYFI 440	
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; Sequence 61, Application US/09944457			
; Patent No. US20020110859A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin			
; APPLICANT: Batson, David			
; APPLICANT: Batson, Dan			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Flivartoff, Ellen			
; APPLICANT: Gerritsen, Mary			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Goddard, Paul			
; APPLICANT: Grimaldi, Christopher			
; APPLICANT: Gurney, Austin			
; APPLICANT: Hillan, Kenneth			
; APPLICANT: Kljavin, Ivar			
; APPLICANT: Napier, Mary			
; APPLICANT: Roy, Margaret			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Wood, William			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P2548P1C1			
; CURRENT APPLICATION NUMBER: US/09/944,457			
; CURRENT FILING DATE: 2001-09-26			
; PRIOR APPLICATION NUMBER: 09/866,028			
; PRIOR FILING DATE: 2001-05-25			
; PRIOR APPLICATION NUMBER: 60/067,411			
; PRIOR FILING DATE: December 3, 1997			
; PRIOR APPLICATION NUMBER: 60/069,334			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,335			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,278			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,425			

; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
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; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-457-61

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Best Local Similarity 99.5%; Pred. No. 3.4e-175;
Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MASVVLPGSSQCAAAAAAAPGLRLRLLLLSAALIPITGDGQNLFTKDVTVIEGEVA 60
Db 1 MASVVLPGSSQCAAAAAAAPG--LRULLLLLSAALIPITGDGQNLFTKDVTVIEGEVA 58
QY 61 TISCQVNSKSDSVIQLLNPNRQTIYFRDPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 120
Db 59 TISCQVNSKSDSVIQLLNPNRQTIYFRDPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 118
QY 121 RYFCQLYTDPPQESYTTITVLVPPRLNMLDIOKTAAGEELEVACTAMASKPATIIEWF 180
Db 119 RYFCQLYTDPPQESYTTITVLVPPRLNMLDIOKTAAGEELEVACTAMASKPATIIEWF 178
QY 181 KGNTELKKGKSEVEENSDMYTIVTSQMLKVKHKDDGVPVICQVEHPAVTGNLTQRYLEVQ 240
Db 179 KGNTELKKGKSEVEENSDMYTIVTSQMLKVKHKDDGVPVICQVEHPAVTGNLTQRYLEVQ 238
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDDEMPQHAVLSGPNLFI 300
Db 239 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVRVDDDEMPQHAVLSGPNLFI 298
QY 301 NNINKTDNGTYRCEASNVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTLTID 360
Db 299 NNINKTDNGTYRCEASNVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTLTID 358
QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFVAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
Db 359 SRAGEGSIKRAVDHAVIGGVAVVVFVAMCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
QY 421 DTAIINAEQGGQNNSEKKEYFI 442
Db 419 DTAIINAEQGGQNNSEKKEYFI 440

RESULT 11
US-09-944-449-61
; Sequence 61, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944.449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,236
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-449-61

Query Match 99.1%; Score 2263; DB 9; Length 440;
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Db 61 TISCQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
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Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
QY 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVKHKKDDGVPVICQVEHPAVTGNLQTOXYLEVQ 240
Db 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVKHKKDDGVPVICQVEHPAVTGNLQTOXYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVWVVDDEMPQHAVLSGPNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVWVVDDEMPQHAVLSGPNLFI 300
QY 301 NNLNKTNDGTYRCASNIYVKAHSDYMLYVYDPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLNKTNDGTYRCASNIYVKAHSDYMLYVYDPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
QY 361 SRAGEGSIRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
QY 421 DTAIINAEQGQNNSEKKEYFI 442
Db 421 DTAIINAEQGQNNSEKKEYFI 442
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RESULT 9

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US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110
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Query Match 99.9%; Score 2280; DB 15; Length 442;
Best Local Similarity 99.8%; Pred. No. 1.4e-176;
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASVLPFSGSQCAAAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEGEVA 60
Db 1 MASVLPFSGSQCAAAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEGEVA 60
QY 61 TISCQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
Db 61 TISCQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLNFSSELKVSILTNVSIISDEG 120
QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEIEVNCCTAMASKPATTTIRWF 180
QY 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVKHKKDDGVPVICQVEHPAVTGNLQTOXYLEVQ 240
Db 181 KGNTLKGKSEVESEWSDMYTVTSQMLKVKHKKDDGVPVICQVEHPAVTGNLQTOXYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVWVVDDEMPQHAVLSGPNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQPMVTVWVVDDEMPQHAVLSGPNLFI 300
QY 301 NNLNKTNDGTYRCASNIYVKAHSDYMLYVYDPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLNKTNDGTYRCASNIYVKAHSDYMLYVYDPTTIPPPPTTTTTTTTTTTTTTTTTITD 360
QY 361 SRAGEGSIRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420
QY 421 DTAIINAEQGQNNSEKKEYFI 442
Db 421 DTAIINAEQGQNNSEKKEYFI 442
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RESULT 10

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US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020059309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61
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Query Match

99.1%; Score 2263; DB 9; Length 440;

Db 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPGDCGNLFTKDVTVIEGEVA 60
Qy 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSITNVSISDEG 120
Db 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSITNVSISDEG 120
Qy 121 RYFCQLYTDPQESYTTITVLVPPRNLMIDIKDTAVEGEIEVNCNTAMASKPATIRWF 180
Db 121 RYFCQLYTDPQESYTTITVLVPPRNLMIDIKDTAVEGEIEVNCNTAMASKPATIRWF 180
Qy 181 KGNTLKGKSEVEWSMDYTTVTSOLMLKVHKEDDGVVICOVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVEWSMDYTTVTSOLMLKVHKEDDGVVICOVEHPAVTGNLQORYLEVQ 240
Qy 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
Qy 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Qy 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Qy 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 7

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/10/403.107
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPGDCGNLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPGDCGNLFTKDVTVIEGEVA 60
Qy 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSITNVSISDEG 120
Db 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSITNVSISDEG 120
Qy 121 RYFCQLYTDPQESYTTITVLVPPRNLMIDIKDTAVEGEIEVNCNTAMASKPATIRWF 180
Db 121 RYFCQLYTDPQESYTTITVLVPPRNLMIDIKDTAVEGEIEVNCNTAMASKPATIRWF 180
Qy 181 KGNTLKGKSEVEWSMDYTTVTSOLMLKVHKEDDGVVICOVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVEWSMDYTTVTSOLMLKVHKEDDGVVICOVEHPAVTGNLQORYLEVQ 240

Qy 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
Qy 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Db 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTITD 360
Qy 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVIGGVAVVAVFAMCLLLIILGRYPARHKGTYPTHEAKGADDAADA 420
Qy 421 DTAINAEGGQNNSEKKEYFI 442
Db 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 8

US-10-015-115-111
; Sequence 113, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111

Query Match 100.0%; Score 2283; DB 15; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPGDCGNLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLLSAALIPGDCGNLFTKDVTVIEGEVA 60
Qy 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSITNVSISDEG 120

RESULT 4

US-09-836-353A-136
; Sequence 136, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF48951
; CURRENT APPLICATION NUMBER: US/09/836.353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-136

Query Match 100.0%; Score 2283; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAAL	PTGQNL	FTKDV	TVIEGEVA	60
DB	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAAL	PTGQNL	FTKDV	TVIEGEVA	60
QY	61	TISCOV	KSDSVIQL	NPQRQ	TIYFR	DRPLK	DSRFP	QLN	FSSELK	VSLTN
DB	61	TISCOV	KSDSVIQL	NPQRQ	TIYFR	DRPLK	DSRFP	QLN	FSSELK	VSLTN
QY	121	RYFCQ	LYTDP	PQBSY	TTIVL	VP	PNLM	DIQ	KTAVE	GEIEI
DB	121	RYFCQ	LYTDP	PQBSY	TTIVL	VP	PNLM	DIQ	KTAVE	GEIEI
QY	181	KGNTL	KGKSE	VEWSD	MTVT	VSQ	MLK	VHK	EDD	GVFV
DB	181	KGNTL	KGKSE	VEWSD	MTVT	VSQ	MLK	VHK	EDD	GVFV
QY	241	YKQV	HIQ	MTY	PLQ	GLT	REG	DAL	ELT	CEA
DB	241	YKQV	HIQ	MTY	PLQ	GLT	REG	DAL	ELT	CEA
QY	301	NNL	NK	TDNG	TYR	CEAS	NI	V	GK	ASD
DB	301	NNL	NK	TDNG	TYR	CEAS	NI	V	GK	ASD
QY	361	SRAGE	SGS	IRAV	DH	AVIG	GVV	AVV	FAM	L
DB	361	SRAGE	SGS	IRAV	DH	AVIG	GVV	AVV	FAM	L
QY	421	DTAI	INAE	GQ	NN	SE	KE	YFI	442	
DB	421	DTAI	INAE	GQ	NN	SE	KE	YFI	442	

RESULT 5

US-10-363-616-262
; Sequence 262, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hveeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363.616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 262
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-262

Query Match 100.0%; Score 2283; DB 12; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAAL	PTGQNL	FTKDV	TVIEGEVA	60
DB	1	MASVLP	SGSQCAAAAAA	PPGLRLRL	LLLLL	PSAAAL	PTGQNL	FTKDV	TVIEGEVA	60
QY	61	TISCOV	KSDSVIQL	NPQRQ	TIYFR	DRPLK	DSRFP	QLN	FSSELK	VSLTN
DB	61	TISCOV	KSDSVIQL	NPQRQ	TIYFR	DRPLK	DSRFP	QLN	FSSELK	VSLTN
QY	121	RYFCQ	LYTDP	PQBSY	TTIVL	VP	PNLM	DIQ	KTAVE	GEIEI
DB	121	RYFCQ	LYTDP	PQBSY	TTIVL	VP	PNLM	DIQ	KTAVE	GEIEI
QY	181	KGNTL	KGKSE	VEWSD	MTVT	VSQ	MLK	VHK	EDD	GVFV
DB	181	KGNTL	KGKSE	VEWSD	MTVT	VSQ	MLK	VHK	EDD	GVFV
QY	241	YKQV	HIQ	MTY	PLQ	GLT	REG	DAL	ELT	CEA
DB	241	YKQV	HIQ	MTY	PLQ	GLT	REG	DAL	ELT	CEA
QY	301	NNL	NK	TDNG	TYR	CEAS	NI	V	GK	ASD
DB	301	NNL	NK	TDNG	TYR	CEAS	NI	V	GK	ASD
QY	361	SRAGE	SGS	IRAV	DH	AVIG	GVV	AVV	FAM	L
DB	361	SRAGE	SGS	IRAV	DH	AVIG	GVV	AVV	FAM	L
QY	421	DTAI	INAE	GQ	NN	SE	KE	YFI	442	
DB	421	DTAI	INAE	GQ	NN	SE	KE	YFI	442	

RESULT 6

US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US2003014478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302.041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778.510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match 100.0%; Score 2283; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 8.1e-177;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLP

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RESULT 2
US-09-778-187B-2
; Sequence 2, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 442
; TYPE: PRT
; ORGANISM: homo sapiens
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; Sequence 136, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 136
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-136
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Best Local Similarity 100.0%; Pred. No. 8.1e-177;
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Db 421 DTAINAEGGQNNSEKKEYFI 442
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 37.5504 Seconds
(without alignments)
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Title: US-09-778-187b-2

Perfect score: 2283

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2283	100.0	442	10	US-09-836-353A-136
5	2283	100.0	442	12	US-10-363-616-262
6	2283	100.0	442	14	US-10-302-041-20
7	2283	100.0	442	14	US-10-403-107-1
8	2283	100.0	442	15	US-10-015-115-111
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19	2263	99.1	440	9	US-09-943-762-61	Sequence 61, Appl
20	2263	99.1	440	9	US-09-944-654-61	Sequence 61, Appl
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27	2263	99.1	440	9	US-09-944-907-61	Sequence 61, Appl
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37	2263	99.1	440	12	US-10-201-853-34	Sequence 34, Appl
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ALIGNMENTS

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; Sequence 20, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

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XX	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;	
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KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;	
KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.	
XX	Homo sapiens.	
XX	W0200168848-A2.	
PN	20-SEP-2001.	
PD	28-FEB-2001; 2001WO-US006520.	
PF	01-MAR-2000; 2000WO-US005601.	
XX	02-MAR-2000; 2000WO-US005841.	
PR	03-MAR-2000; 2000US-0187202P.	
PR	06-MAR-2000; 2000US-0186968P.	
PR	14-MAR-2000; 2000US-0189320P.	
PR	14-MAR-2000; 2000US-0189328P.	
PR	15-MAR-2000; 2000WO-US006884.	
PR	21-MAR-2000; 2000US-0190828P.	
PR	21-MAR-2000; 2000US-0191007P.	
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PR	21-MAR-2000; 2000US-0191314P.	
PR	28-MAR-2000; 2000US-0192655P.	

PR	29-MAR-2000; 2000US-0193032P.	
PR	29-MAR-2000; 2000US-0193053P.	
PR	30-MAR-2000; 2000WO-US008439.	
PR	04-APR-2000; 2000US-0194449P.	
PR	04-APR-2000; 2000US-0194647P.	
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PR	25-APR-2000; 2000US-0199550P.	
PR	25-APR-2000; 2000US-0199654P.	
PR	03-MAY-2000; 2000US-0201516P.	
PR	17-MAY-2000; 2000WO-US013705.	
PR	22-MAY-2000; 2000WO-US014042.	
PR	30-MAY-2000; 2000WO-US014941.	
PR	02-JUN-2000; 2000WO-US015264.	
PR	05-JUN-2000; 2000US-0209832P.	
PR	28-JUL-2000; 2000WO-US020710.	
PR	22-AUG-2000; 2000US-00644848.	
PR	24-AUG-2000; 2000WO-US033328.	
PR	08-NOV-2000; 2000WO-US030952.	
PR	01-DEC-2000; 2000WO-US032678.	
PR	20-DEC-2000; 2000WO-US034956.	
XX	(GETH) GENENTECH INC.	
PA	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;	
XX	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;	
PI	WPI; 2001-602746/68.	
DR	N-PSDB; AAS45941.	
XX	Novel nucleic acids encoding PRO polypeptides, used to diagnose the	
PT	presence of tumors, such as prostate and breast tumors, in mammals and to	
PT	screen for modulators of the compounds.	
XX	Claim 11; Fig 34; 774pp; English.	
PS	Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.	
XX	The PRO polypeptides and their associated nucleic acids can be used to	
CC	detect the presence of a tumour in a mammal by comparing the level of	
CC	expression of a PRO polypeptide in a test sample of cells from the animal	
CC	and a control sample of normal cells, whereby a higher level of	
CC	expression in the test sample indicates the presence of a tumour in the	
CC	mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats	
CC	and rabbits but are preferably human. The polypeptides can be used to	
CC	stimulate tumour necrosis factor (TNF) alpha release from human blood,	
CC	when contacted with it. A specific polypeptide can be used to stimulate	
CC	the proliferation or differentiation of chondrocyte cells. The PRO	
CC	proteins can be used to determine the presence of tumours and also	
CC	susceptibility to tumour development, particularly adrenal, lung, colon,	
CC	breast, prostate, rectal, cervical, or liver tumours, in mammalian	
CC	subjects. The oligonucleotide probes specific for the PRO nucleic acids	
CC	can be used for genetic analysis of individuals with genetic disorders	
XX	Sequence 440 AA;	
SQ	Query Match	99.1%; Score 2263; DB 4; Length 440;
	Best Local Similarity	99.5%; Pred. No. 1.7e-156;
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AC ADE61608;
XX 29-JAN-2004 (first entry)
XX Human Protein AAF69029, SEQ ID NO 7528.
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX W02003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GHEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-269312/26.
XX GENBANK; AAF69029.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
XX human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 442 AA;
XX
XX Query Match 99.9%; Score 2280; DB 7; Length 442;
XX Best Local Similarity 99.8%; Pred. No. 9.6e-158;
XX Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MASVVLPSGSCAAAAAAPGRLRLRLLLLSAALIPGTGQCNLFKDVTVIEGEVA 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 MASVVLPSGSCAAAAAAPGRLRLRLLLLSAALIPGTGQCNLFKDVTVIEGEVA 60

QY 61 TISCQVKNKSDSDSVIQLLNPNROTIIYFRDPRPLKDSRFQLLNFSSELKVLSTNVSISDEG 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
61 TISCQVKNKSDSDSVIQLLNPNROTIIYFRDPRPLKDSRFQLLNFSSELKVLSTNVSISDEG 120
QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEEIEVNCTANASKPATIRWF 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEEIEVNCTANASKPATIRWF 180
QY 181 KGNTLKGKSEVEEWSDMYTVTSQMLMKVHKEDDGVFVICOVEHPAVTGNLQRYLEYQ 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
181 KGNTLKGKSEVEEWSDMYTVTSQMLMKVHKEDDGVFVICOVEHPAVTGNLQRYLEYQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKPOPMVMTWVRVDDMPQHAVLSGNLFI 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKPOPMVMTWVRVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTT 360
QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTPTTHEAKGADDAADA 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTPTTHEAKGADDAADA 420
QY 421 DTAIINAEQGNNSSEKKEYFI 442
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
421 DTAIINAEQGNNSSEKKEYFI 442
RESULT 13
AAV17830
ID AAV17830 standard; protein; 440 AA.
XX AC AAV17830;
XX DT 12-AUG-1999 (first entry)
XX DE Human PRO355 protein sequence.
XX KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
XX secreted protein; transmembrane protein; inflammation disorder.
XX OS Homo sapiens.
XX PN W09928462-A2.
XX PD 10-JUN-1999.
XX PF 01-DEC-1998; 98WO-US025108.
XX PR 03-DEC-1997; 97US-0067411P.
XX PR 11-DEC-1997; 97US-0069278P.
XX PR 11-DEC-1997; 97US-0069334P.
XX PR 12-DEC-1997; 97US-0069425P.
XX PR 16-DEC-1997; 97US-0069694P.
XX PR 16-DEC-1997; 97US-0069696P.
XX PR 17-DEC-1997; 97US-0069702P.
XX PR 17-DEC-1997; 97US-0069870P.
XX PR 18-DEC-1997; 97US-0069873P.
XX PR 05-JAN-1998; 98US-0070440P.
XX PR 03-FEB-1998; 98US-0074086P.
XX PR 03-FEB-1998; 98US-0074092P.
XX PR 25-FEB-1998; 98US-0075945P.
XX (GETH) GENENTECH INC.
XX PA Wood WL, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
XX WPI; 1999-371118/31.
XX N-PSDB; AAX80055.
XX

Best Local Similarity 99.8%; Pred. No. 9.6e-158;		
Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MASVVLPSGSCAAAAAAPPGLRLRLLLLLLSAAALIPTGQGNLFTKDVTVIEGEVA 60	
Db	1 MASVVLPSGSCAAAAAAPPGLRLRLLLLLLSAAALIPTGQGNLFTKDVTVIEGEVA 60	
QY	61 TISCQVKNKSDSVIQLLNPNRQTIYFRDPLKDSRFQLNPFSSSELKVSLTNVSIISDEG 120	
Db	61 TISCQVKNKSDSVIQLLNPNRQTIYFRDPLKDSRFQLNPFSSSELKVSLTNVSIISDEG 120	
QY	121 RYFCQLYTDPPQSYTTITVLVPPRNLMIDIKQDAVEGEIEVNCCTAMASKPATTTIRWF 180	
Db	121 RYFCQLYTDPPQSYTTITVLVPPRNLMIDIKQDAVEGEIEVNCCTAMASKPATTTIRWF 180	
QY	181 KGTELKKGKSEVEEWSDMYTVTTSQMLMKVHKHDDGVPVICQVEHPAVTGNLQTORYLEVQ 240	
Db	181 KGTELKKGKSEVEEWSDMYTVTTSQMLMKVHKHDDGVPVICQVEHPAVTGNLQTORYLEVQ 240	
QY	241 YKQVHIQMTYPLQGLTREGDALELTCEALGKGPQVMVTVRVVDDEMPQHAVLSGPNLFI 300	
Db	241 YKQVHIQMTYPLQGLTREGDALELTCEALGKGPQVMVTVRVVDDEMPQHAVLSGPNLFI 300	
QY	301 NNLKNTDNGTYRCBASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTIITD 360	
Db	301 NNLKNTDNGTYRCBASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTTIITD 360	
QY	361 SRAGEEGSIRAVDHAVIGGVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420	
Db	361 SRAGEEGSIRAVDHAVIGGVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADA 420	
QY	421 DTAIINAEGGQNNSEKKEYFI 442	
Db	421 DTAIINAEGGQNNSEKKEYFI 442	
RESULT 11		
ADE61605		
ID	ADE61605 standard; protein; 442 AA.	
XX	ADE61605;	
XX		
DT	29-JAN-2004 (first entry)	
XX	Human Protein AAF69029, SEQ ID NO 7525.	
XX	Human; pain; neuronal tissue; gene therapy;	
KW	spinal segmental nerve injury; chronic constriction injury; CCI;	
KW	spared nerve injury; SNI; Chung.	
XX	Homo sapiens.	
OS	WO2003016475-A2.	
PN	27-FEB-2003.	
PD		
PF	14-AUG-2002; 2002WO-US025765.	
XX		
XX	14-AUG-2001; 2001US-0312147P.	
PR	01-NOV-2001; 2001US-0346382P.	
PR	26-NOV-2001; 2001US-0333347P.	
XX		
XX	(GEHO) GEN HOSPITAL CORP.	
PA	(FARB) BAYER AG.	
XX		
PI	Woolf C, D'urso D, Belfort K, Costigan M;	
XX		
DR	WPI; 2003-268312/26.	
DR	GENBANK; AAF69029.	
XX		
PT	New composition comprising two or more isolated polypeptides, useful for	
PT	preparing a medicament for treating pain in an animal.	
XX		

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published/pct_sequences](http://wipo.int/pub/published/pct_sequences).

Sequence 442 AA;

Query Match	99.9%;	Score 2280;	DB 7;	Length 442;
Best Local Similarity	99.8%;	Pred. No. 9.6e-158;		
Matches 441;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

```

Qy 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPITGDGQNLFTKDVVIEGEVA 60
Db 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPITGDGQNLFTKDVVIEGEVA 60

Qy 61 TISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFOLLNFSSELKVSLTNVSISDBG 120
Db 61 TISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFOLLNFSSELKVSLTNVSISDBG 120

Qy 121 RYFCQLYDPPQBSYTIITVLVPPRNLMDIQKDTAVEGEIEVNVCTAMASKPATIRWF 180
Db 121 RYFCQLYDPPQBSYTIITVLVPPRNLMDIQKDTAVEGEIEVNVCTAMASKPATIRWF 180

Qy 181 KGNTLKGKSEVBWSDMYVTQSOLMLKVHKEDDGPVVICQVEHPAVTGNLQORYLEVQ 240
Db 181 KGNTLKGKSEVBWSDMYVTQSOLMLKVHKEDDGPVVICQVEHPAVTGNLQORYLEVQ 240

Qy 241 YKQVQHVMQTYPLQGLTREGDALELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGPNLFI 300
Db 241 YKQVQHVMQTYPLQGLTREGDALELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGPNLFI 300

Qy 301 NNLNKTDMGTYRCEASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360
Db 301 NNLNKTDMGTYRCEASNIVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTTTTT 360

Qy 361 SRAGEEGSIRAVDHAVTGGVVAVVVFVAMLCILIIILGRYFASHKGTFTYHEAKGADAADA 420
Db 361 SRAGEEGSIRAVDHAVTGGVVAVVVFVAMLCILIIILGRYFASHKGTFTYHEAKGADAADA 420

Qy 4421 DTALINAEGGONNSEEXKEYFI 442
Db 4421 DTALINAEGGONNSEEXKEYFI 442

```

RESULT 12
ADE61608
ID ADE61608 standard; protein; 442 AA.
XX

Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPVMVTVWRVDDMPQHAVLSGNLFI 300
 QY 301 NNLNKTDNGTYRCEASNIYKAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTTTTTIITD 360
 Db 301 NNLNKTDNGTYRCEASNIYKAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTTTTTIITD 360
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 Db 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 QY 421 DTAIINAEQGNNSSEKKEYFI 442
 Db 421 DTAIINAEQGNNSSEKKEYFI 442

RESULT 8
 ADE86685
 ID ADE86685 standard; protein; 442 AA.
 AC ADE86685;
 DT 29-JAN-2004 (first entry)
 DE Novel human secreted protein #11 associated protein #1.
 XX human; secreted protein; cancer; liver disorder; hepatitis;
 KW neural disorder; Alzheimer's disease.
 XX Homo sapiens.
 XX US2003129685-A1.
 XX 10-JUL-2003.
 XX 18-APR-2001; 2001US-00836353.
 XX 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 XX (NIJ/J) NI J.
 PA (YOUNG) YOUNG P E.
 PA (KENN) KENNY J J.
 PA (OLSE) OLSEN H S.
 PA (MOOR) MOORE P A.
 PA (WEIY) WEI Y.
 PA (GREE) GREENE J M.
 PA (RUBE) RUBEN S M.
 XX Ni J, Young PE, Kenny JU, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM;
 XX WPI; 2004-020335/02.
 DR New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX Disclosure; SEQ ID NO 136; 380pp; English.
 PS The invention relates to an isolated nucleic acid sequence, or its
 CC allelic variant, a fragment of the cDNA sequence, or its fragment,
 CC domain, epitope or species homologue. The nucleic acid is useful for
 CC preparing a medicament for preventing, treating or ameliorating a medical
 CC condition e.g., cancer, liver disorders such as hepatitis or neural
 CC disorders such as Alzheimer's disease. The present sequence represents
 CC the amino acid sequence of a novel human secreted protein associated
 CC protein.
 XX Sequence 442 AA;
 SQ Query Match 100.0%; Score 2283; DB 8; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;

Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASVLPSCGCAAAAAAAPPGLRLRLRLLLLSAALPTGQGNLFTKQDVTVIGEVA 60
 Db 1 MASVLPSCGCAAAAAAAPPGLRLRLRLLLLSAALPTGQGNLFTKQDVTVIGEVA 60
 QY 61 TISCQVNSDDSDVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKYSLTNVSISDEG 120
 Db 61 TISCQVNSDDSDVIQLNPNRQTIYFRDPRPLKDSRFQLNFSSELKYSLTNVSISDEG 120
 QY 121 RYFCQLYTDPQESYTTITVLVPPRNLMDIOKDTAVEGEIEVNCAMASKPATIRWF 180
 Db 121 RYFCQLYTDPQESYTTITVLVPPRNLMDIOKDTAVEGEIEVNCAMASKPATIRWF 180
 QY 181 KGNTLKGKSEVEEWSMDMTVTISQLMLKVHKEDDGVFVICOVEHPAVTGNLQRYLEVQ 240
 Db 181 KGNTLKGKSEVEEWSMDMTVTISQLMLKVHKEDDGVFVICOVEHPAVTGNLQRYLEVQ 240
 QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPVMVTVWRVDDMPQHAVLSGNLFI 300
 Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPVMVTVWRVDDMPQHAVLSGNLFI 300
 QY 301 NNLNKTDNGTYRCEASNIYKAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTIITD 360
 Db 301 NNLNKTDNGTYRCEASNIYKAHSDYMLVYDPTTIPPPPTTTTTTTTTTTTTIITD 360
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 Db 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 QY 421 DTAIINAEQGNNSSEKKEYFI 442
 Db 421 DTAIINAEQGNNSSEKKEYFI 442

RESULT 9
 ABO07196
 ID ABO07196 standard; protein; 442 AA.
 XX ABO07196;
 XX 13-AUG-2003 (first entry)
 DT Human p53 modifying protein, SEQ ID 156.
 DE Human p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 XX antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.
 XX Homo sapiens.
 OS WO2002099122-A1.
 PN 12-DEC-2002.
 PD 03-JUN-2002; 2002WO-US017382.
 XX 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX (EXEL-) EXELIXIS INC.
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI WPI; 2003-156859/15.
 DR N-PSDB; ACD13371.
 DR Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.

CC in a biological assay and identifying the protein in the supernatant
 CC having the activity). The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation and other immune
 CC disorders, neurological and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

XX
 XX
 SQ Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 6; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLFSAALIPDGDQNLFTKDVTVIEGEVA 60
 DB |||||
 QY 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLFSAALIPDGDQNLFTKDVTVIEGEVA 60
 DB |||||
 QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKSLTNVSIISDEG 120
 DB |||||
 QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKSLTNVSIISDEG 120
 DB |||||
 QY 121 RYFCQLYTDPQESYTTITVLVPPNRLMIDIQKDTAVEGEIEVNCNTAMASKATTIRWF 180
 DB |||||
 QY 121 RYFCQLYTDPQESYTTITVLVPPNRLMIDIQKDTAVEGEIEVNCNTAMASKATTIRWF 180
 DB |||||
 QY 181 KGNTELKGKSEVEEWSDMYTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTVIEVQ 240
 DB |||||
 QY 181 KGNTELKGKSEVEEWSDMYTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTVIEVQ 240
 DB |||||
 QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFI 300
 DB |||||
 QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFI 300
 DB |||||
 QY 301 NNLKTONGTYRCEASNVGKHSYMLVYVDPPTTTPPTTTTITTTTITTTTITTTIT 360
 DB |||||
 QY 301 NNLKTONGTYRCEASNVGKHSYMLVYVDPPTTTPPTTTTITTTTITTTTITTTIT 360
 DB |||||
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCILILGRIYFAHKGTYFTHEAKGADDAADA 420
 DB |||||
 QY 361 SRAGEGSIKRAVDHAVIGGVAVVVFAMLCILILGRIYFAHKGTYFTHEAKGADDAADA 420
 DB |||||
 QY 421 DTALINAEQGQNNSEKKEYFI 442
 DB |||||
 QY 421 DTALINAEQGQNNSEKKEYFI 442
 DB |||||

RESULT 7

AD54238

ID ADE54238 standard; protein; 442 AA.

XX ADE54238;

XX AC

XX DT

XX 29-JAN-2004 (first entry)

DE Human Protein NP_055148, SEQ ID NO 41.

XX Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS

XX W02003016475-A2.

FN

XX

PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2C03-268312/26.

XX GENBANK; NP_055148.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 442 AA;

QY Query Match 100.0%; Score 2283; DB 7; Length 442;

DB Best Local Similarity 100.0%; Pred. No. 5.8e-158;

QY Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLFSAALIPDGDQNLFTKDVTVIEGEVA 60

DB |||||

QY 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLFSAALIPDGDQNLFTKDVTVIEGEVA 60

DB |||||

QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKSLTNVSIISDEG 120

DB |||||

QY 61 TISCQVNSDSDSVIQLNPNRQTIYFRDPLKDSRFQNLNFSSELKSLTNVSIISDEG 120

DB |||||

QY 121 RYFCQLYTDPQESYTTITVLVPPNRLMIDIQKDTAVEGEIEVNCNTAMASKATTIRWF 180

DB |||||

QY 121 RYFCQLYTDPQESYTTITVLVPPNRLMIDIQKDTAVEGEIEVNCNTAMASKATTIRWF 180

DB |||||

QY 181 KGNTELKGKSEVEEWSDMYTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTVIEVQ 240

DB |||||

QY 181 KGNTELKGKSEVEEWSDMYTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQTVIEVQ 240

DB |||||

QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMTWVRVDDEMPQHAVLSGPNLFI 300

DB |||||

XX PD 07-MAR-2002.
XX PF 31-AUG-2001; 2001WO-US027093.
XX PR 01-SEP-2000; 2000US-00654935.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
XX DR WPI; 2002-583321/62.
XX DR N-PSDB; ABQ93304.
XX PT New polynucleotide and polypeptides, useful for treatment and diagnosis
XX PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
XX PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
XX PT sclerosis, diabetes and allergies.
XX PS Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English.
XX CC The invention relates to an isolated polynucleotide (I) comprising one of
XX CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
XX CC administering to a mammalian subject a composition comprising the protein
XX CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
XX CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
XX CC (I) is useful for gene therapy of diseases and (II) can be used for
XX CC therapeutic treatment. Diseases that may be treated include wound healing
XX CC and tissue repair, burns, central nervous system disorders (e.g.
XX CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
XX CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
XX CC sclerosis, diabetes and allergies. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX CC Sequence 442 AA;
XX SQ

Query Match 100.0%; Score 2283; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.8e-158;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60
Db 1 MASVVLPSGSCAAAAAAPPGLRLRLRLLLFSAALIPFGDQNLFTKDVTVIEGEVA 60

QY 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVLSTNVSISDEG 120
Db 61 TISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSELKVLSTNVSISDEG 120

QY 121 RYFCQLYTDPQESYTTITVLVPPNLMIDIQDXTAVEGEEIEVNCNTAMASKPATIRWF 180
Db 121 RYFCQLYTDPQESYTTITVLVPPNLMIDIQDXTAVEGEEIEVNCNTAMASKPATIRWF 180

QY 181 KGNTELKGESEVSEWSDMYVTSQMLKVKHEDGVPVICOVEHPATVGNLQRYLEVQ 240
Db 181 KGNTELKGESEVSEWSDMYVTSQMLKVKHEDGVPVICOVEHPATVGNLQRYLEVQ 240

QY 241 YKPOVHIQMTYPLQGLTREGDALELTCAIGKPPQVWVWVRVDEMPQHAVLSGPNLFI 300
Db 241 YKPOVHIQMTYPLQGLTREGDALELTCAIGKPPQVWVWVRVDEMPQHAVLSGPNLFI 300

QY 301 NNLKNTONGTYRCASINIVGKASDYMVLVYDPTTIPPTTTTTTTTTTTTTTTTTITD 360
Db 301 NNLKNTONGTYRCASINIVGKASDYMVLVYDPTTIPPTTTTTTTTTTTTTTTTTITD 360

QY 361 SRAGEGSIRAVDHAVTGGVAVVAVFAMLCILLIILGYFARHKGTFTTHEAKGADDAADA 420
Db 361 SRAGEGSIRAVDHAVTGGVAVVAVFAMLCILLIILGYFARHKGTFTTHEAKGADDAADA 420

QY 442 DTALINAEGGQNNSEKKEYFI 442
Db 442 DTALINAEGGQNNSEKKEYFI 442

Db 421 DTALINAEGGQNNSEKKEYFI 442

RESULT 6
ADA27144
ID ADA27144 standard; protein; 442 AA.
XX AC ADA27144;
XX DT 20-NOV-2003 (first entry)
XX DE Human novel secreted protein from gene 11 #3.
XX KW cytostatic; antiinflammatory; immunomodulator; neuroprotective;
XX KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
XX KW neurological disorder; blood clotting disorder; food additive;
XX KW preservative; human; secreted protein.
XX OS Homo sapiens.
XX PN US2003055231-A1.
XX PD 20-MAR-2003.
XX PF 29-OCT-2001; 2001US-00984130.
XX PR 28-OCT-1998; 98US-0105971P.
XX PR 27-OCT-1999; 99WO-US025031.
XX PR 19-APR-2000; 2000US-0198407P.
XX PR 30-OCT-2000; 2000US-0243792P.
XX PR 18-APR-2001; 2001US-00836353.
XX PA (NIJ/) NI J.
XX PA (YOUN/) YOUNG P E.
XX PA (KENN/) KENNY J J.
XX PA (OLSE/) OLSEN H S.
XX PA (MOOR/) MOORE P A.
XX PA (WEIY/) WEI Y.
XX PA (GREE/) GREENE J M.
XX PA (RUBE/) RUBEN S M.
XX PA (LIUD/) LIU D.
XX PA (CROC/) CROCKER P R.
XX PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
PI Ruben SM, Liu D, Crocker PR;
XX WPI; 2003-567103/53.
XX PT New human secreted nucleic acid molecules and polypeptides, useful for
XX PT preventing, treating, or ameliorating a medical condition, such as
XX PT cancer, inflammation, immune disorders, neurological and blood clotting
XX PT disorders.
XX PS Disclosure; Page 72; 454pp; English.
XX CC The invention relates to an isolated nucleic molecule that is at least
XX CC 9% identical to 18 human cDNA sequences representing 12 novel genes
XX CC encoding secreted proteins or a polynucleotide fragment of the cDNA
XX CC sequence contained in American Type Culture Collection (ATCC) deposit No.
XX CC defined in the specification, its species homologue, a variant or allelic
XX CC variant of the polynucleotide having a polynucleotide capable of
XX CC hybridising under conditions the polynucleotide, where the polynucleotide
XX CC does not hybridise under stringent conditions to a nucleic acid molecule
XX CC having a nucleotide sequence of only A or T residues. Also included are
XX CC recombinant vectors, host cells (for producing the polypeptide), the
XX CC secreted polypeptide (comprising a sequence that is at least 95%
XX CC identical to a polypeptide fragment, domain, epitope, full-length
XX CC protein, variant, allelic variant or species homologue), antibodies that
XX CC specifically bind to the polypeptides, diagnosing, treating, preventing
XX CC or ameliorating a medical condition by administering the polynucleotide
XX CC or the polypeptide, the gene corresponding to the cDNA sequence and
XX CC identifying an activity in a biological assay (by expressing the cDNA
XX CC sequence in a cell, isolating the supernatant, and detecting an activity

QY 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
DB 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
QY 61 TISQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 120
DB 61 TISQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 120
QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEEIEVNCVTAMASKPATIRWF 180
DB 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEEIEVNCVTAMASKPATIRWF 180
QY 181 KGNTELKKGSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
DB 181 KGNTELKKGSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTITTTTITTTITTTIT 360
DB 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTITTTTITTTITTTIT 360
QY 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGYTFTHAKGADDAADA 420
DB 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGYTFTHAKGADDAADA 420
QY 421 DTAINAEGGQNNSEKKEYFI 442
DB 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 4
AAE19887
ID AAE19887 standard; protein; 442 AA.
AC AAE19887;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
XX
KW Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KW liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200214557-A1.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025690.
XX
PR 15-AUG-2000; 2000US-0225264P.
XX
PA (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
FI Reeves RH, Yoshinori M;
XX
DR WPI; 2002-241913/29.
XX
PT Detecting cell proliferative disorder associated with tumor suppressor
PT lung cancer (TSLC1) in subject, comprises contacting proliferating cell
PT of subject with reagent detecting TSLC1 and detecting modification in
PT TSLC1 level.
XX
PS Disclosure; Page 49-50; 59pp; English.
XX
CC The invention relates to a method for detecting cell proliferative
CC disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a

CC subject. The method comprising contacting a cell component of a
CC proliferating cell with a reagent that detects level of the cell
CC component in the proliferating cell and determining modification in the
CC level of the cell component in proliferating cell as compared with a
CC healthy cell, where modification indicates disorder associated with a
CC TSLC1. The method is useful for detecting a cell proliferative disorder
CC (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
CC lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
CC therapy and for treating a cell proliferative disorder such as lung
CC cancer (human non-small cell lung cancer), liver cancer (hepatocellular
CC carcinoma) or pancreatic cancer associated with modification of TSLC1
CC production, where a reagent which modulates (preferably, increases) TSLC1
CC level in the cells, is employed. The present sequence is human TSLC1
XX
SQ Sequence 442 AA;
Query Match 100.0%; Score 2283; DB 5; Length 442;
Best Local Similarity 100.0%; Pred. No. 5.8e-158;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
DB 1 MASVLPSSGQCAAAAAAAPPGLRLRLRLLLLSAAALPTGQGNLFTKQVTVIEGEVA 60
QY 61 TISQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 120
DB 61 TISQVKNKSDSVIQLLNPRTIYFRDPRPLKDSRFQLLNPFSSSELKVSLSNVSISDEG 120
QY 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEEIEVNCVTAMASKPATIRWF 180
DB 121 RYFCQLYTDPPOESYTTITVLVPPRNLMIDIQDTAVEGEEIEVNCVTAMASKPATIRWF 180
QY 181 KGNTELKKGSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
DB 181 KGNTELKKGSEVEEWSDMYTVTSQMLKVHKEDDGVPIQVEHPAVTGNLQRYLEVQ 240
QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
DB 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVRVDDMPQHAVLSGPNLFI 300
QY 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTITTTTITTTITTTIT 360
DB 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTITTTTITTTITTTIT 360
QY 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGYTFTHAKGADDAADA 420
DB 361 SRAGEGSIRAVDHAVIGGVAVVVFAMCLLIILGRYFARHKGYTFTHAKGADDAADA 420
QY 421 DTAINAEGGQNNSEKKEYFI 442
DB 421 DTAINAEGGQNNSEKKEYFI 442

RESULT 5
ABP62825
ID ABP62825 standard; protein; 442 AA.
XX
AC ABP62825;
XX
DT 14-OCT-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 262.
XX
KW Human; vulnary; dermatological; neuroprotective; nootropic; cancer;
KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
KW burn; central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; immune disorder;
KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
OS Homo sapiens.
XX
PN WO2002:8424-A2.

Claim 1; Page 81-82; 97pp; English.

PS The present sequence is a novel human cell surface receptor protein
 CC (HCSR) designated HCSR-8. The nucleotide sequence was identified in
 CC Incyte Clone 312256 from the cDNA library LUNGNOT02, which was made from
 CC RNA isolated from lung tissue. A number of Incyte Clones were used to
 CC assemble the consensus sequence. BLAST analysis showed that the sequence
 CC is homologous to immuno-superfamily protein B12 g3779242. HCSR and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HCSR may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing HCSR
 CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
 CC immunogenic fragments are useful for drug screening using libraries of
 CC compounds

SQ Sequence 442 AA;

Query Match 100.0%; Score 2283; DB 3; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.8e-158;
 Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGQCAAAAAAPPGLRLRLLLLSAALIFTDGQNLFTKDVTVIEGEVA 60
 Db 1 MASVLPSSGQCAAAAAAPPGLRLRLLLLSAALIFTDGQNLFTKDVTVIEGEVA 60

QY 61 TISQVKNKSDSVTLQNLNPNRTIYFRDPLKDSRQOLLNFSSELKVSILTNVISDEG 120
 Db 61 TISQVKNKSDSVTLQNLNPNRTIYFRDPLKDSRQOLLNFSSELKVSILTNVISDEG 120

QY 121 RYFCQLYTDPQPSYTTITVLVPPRNLMIDIQDVAVEGEIEVNCMTAMASKPATITIRWF 180
 Db 121 RYFCQLYTDPQPSYTTITVLVPPRNLMIDIQDVAVEGEIEVNCMTAMASKPATITIRWF 180

QY 181 KGNTLKGKSEVESEWSMTYTTVTSQMLKVHKEDDGVPIQVHEPAVTGNLQTVYLEVQ 240
 Db 181 KGNTLKGKSEVESEWSMTYTTVTSQMLKVHKEDDGVPIQVHEPAVTGNLQTVYLEVQ 240

QY 241 YKQVHIQMTYPIQGLTREGDALELTCEATGKQPVMVTVRVDDEMPQHAVLSGNLFI 300
 Db 241 YKQVHIQMTYPIQGLTREGDALELTCEATGKQPVMVTVRVDDEMPQHAVLSGNLFI 300

QY 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTT 360
 Db 301 NNLKNTDNGTYRCEASNIVGKAHSDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTT 360

QY 361 SRAGEGSTRADVHVGTVGVVAVVVFAMLCILILGRYFARHKGTYPTHEAKGADDAADA 420
 Db 361 SRAGEGSTRADVHVGTVGVVAVVVFAMLCILILGRYFARHKGTYPTHEAKGADDAADA 420

QY 421 DTALINAEQGNNSSEKKEVFI 442
 Db 421 DTALINAEQGNNSSEKKEVFI 442

RESULT 3
 AAY45092

ID AAY45092 standard; protein; 442 AA.

AC AAY45092;

XX 31-MAY-2000 (first entry)

DE Human lymphoid derived dendritic cell adhesion molecule.

XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;

KW B7-L1; T cell proliferation; natural killer cell; NK; tumour cell;

KW

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 50.5888 Seconds
(without alignments)
2468.650 Million cell updates/sec

Title: US-09-778-187B-2

Perfect score: 2283

Sequence: 1 MASVVLPSGSCRAAAAAA.....ALINAGGQNNSEKKEFYI 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	2283	100.0	442	3	AAB25619 Protein e
2	2283	100.0	442	3	AAY94341 Human cel
3	2283	100.0	442	3	AAY45092 Human lym
4	2283	100.0	442	5	AAE19887 Human tum
5	2283	100.0	442	5	ABP62825 Human pol
6	2283	100.0	442	6	ADA27144 Human nov
7	2283	100.0	442	7	ADE54238 Human pro
8	2283	100.0	442	8	ADE86685 Novel hum
9	2280	99.9	442	6	ABO07196 Human p53
10	2280	99.9	442	6	ABO07231 Human p53
11	2280	99.9	442	7	ADE61605 Human pro
12	2280	99.9	442	7	ADE61608 Human pro
13	2263	99.1	440	2	AAY17830 Human pro
14	2263	99.1	440	3	ABO13321 Human pro
15	2263	99.1	440	4	AAU29040 Human pro
16	2263	99.1	440	6	ABU58416 Human pro
17	2263	99.1	440	6	ABU87964 Human pro
18	2263	99.1	440	6	ABU84279 Novel hum
19	2263	99.1	440	6	ABR66153 Human sec
20	2263	99.1	440	6	ABR65543 Human sec
21	2263	99.1	440	6	ABU99483 Human sec
22	2263	99.1	440	6	ABU55930 Human sec
23	2263	99.1	440	6	ABU82722 Human pro
24	2263	99.1	440	6	ABU98843 Novel hum
25	2263	99.1	440	6	ABR68092 Human sec

26	2263	99.1	440	6	ABU96145	Novel hum
27	2263	99.1	440	6	ABU92576	Human sec
28	2263	99.1	440	6	ABO08653	Human sec
29	2263	99.1	440	6	ABO02705	Human sec
30	2263	99.1	440	6	ABR74859	Human sec
31	2263	99.1	440	6	ABR94621	Human sec
32	2263	99.1	440	6	ABU60240	Human PRO
33	2263	99.1	440	6	ABU85594	Human PRO
34	2263	99.1	440	6	ABU98754	Human PRO
35	2263	99.1	440	6	ABU97969	Novel hum
36	2263	99.1	440	6	ABU91675	Novel hum
37	2263	99.1	440	6	ABU89368	Human PRO
38	2263	99.1	440	6	ABU86209	Human sec
39	2263	99.1	440	6	ABU67422	Human sec
40	2263	99.1	440	6	ABU80450	Human PRO
41	2263	99.1	440	6	ABR99368	Human sec
42	2263	99.1	440	6	ABR98758	Human sec
43	2263	99.1	440	6	ABO16281	Human sec
44	2263	99.1	440	6	ABR92181	Human sec
45	2263	99.1	440	6	ABO18822	Human sec

ALIGNMENTS

RESULT 1
AAB25619

ID AAB25619 standard; protein; 442 AA.

AC AAB25619;

XX 21-NOV-2000 (first entry)

XX Protein encoded by human secreted protein gene #11.

DE Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antineumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; vulnery; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human.

XX Homo sapiens.

XX WO200029435-A1.

XX 25-MAY-2000.

XX 27-OCT-1999; 99WO-US025031.

XX 28-OCT-1998; 98US-0105971P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
Greene JM;

XX WPI; 2000-387742/33.

Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.

Disclosure; Page 182-183; 803pp; English.

The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in CC AAA80606-AB0623 encode the 12 secreted protein sequences given in CC AAB25576-B25593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the

```
Db 61 KVHEDDGPVVCQVEHFAVNTGLQRYLEQYKRPQVHIQMTYPLQGLTREGDALELTC 120
Qy 268 EAIGKPPQPMVTVWVRVDDMPHAYLSPGNLFINNLTNDNGTYRCEASNIVGKAHSDYM 327
Db 121 EAIGKPPQPMVTVWVRVDDMPHAYLSPGNLFINNLTNDNGTYRCEASNIVGKAHSDYI 180
Qy 328 LYVYDPTTIPPPPTTTTTTTTTTTTTIIITIIHDSRAGEEGSIRAVDHAVIGGVAVVVA 387
Db 181 LYVYD-----TTATTEPAVHDSRAGEEGTIGAVDHAVIGGVAVVVA 223
Qy 388 MCLLLIILGRYFARHKGTYFTHAKGADDAADATTAIINAEQQNNSEKKEYFI 442
Db 224 MCLLLIILGRYFARHKGTYFTHAKGADDAADATTAIINAEQQNNSEKKEYFI 278

RESULT 15
Q8N3J6 PRELIMINARY; PRT; 435 AA.
ID Q8N3J6
AC Q8N3J6;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP761G128
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgama;
EA Koshner K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG_3.
DR SMART; SMO0409; IG; 2.
DR SMART; SMO0408; IGC2; 2.
DR PROSITE; PS00835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 39.6%; Score 903; DB 4; Length 435;
Best Local Similarity 44.4%; Pred. No. 1.le-68;
Matches 193; Conservative 76; Mismatches 138; Indels 28; Gaps 7;

Qy 29 LLLFSAALIPG-DGNLFTKDVTVIEGVATISQVKNKSDSVIQLLNPNRQTIYFR 87
Db 8 VLRFYSVCGLLQLQSQGFPLTQNVTVVGGTALTCTCRVDNDNTSLQWNPAAQTLYFD 67
Qy 88 DFRFLKDSRFQLNFSSELKSVLTNVSISDEGRYFCQLYTDPQESVTTITVLVPPRL 147
Db 68 DKKALRDNRIELVRASWHELSISVDSVLSDEGQYTCSLFTMPVKTSKAVLTVLGVPEKP 127
Qy 148 MIDIQKTAVEGEIEFVNCAMASKPATIRFWKGNTELKKGSEVEWS---DMYTVTSQ 204
Db 128 QISGFSSPVMEGDLMLQTLCTSGSKPAADIRWFKNDKEIKDKVYLKEEDANRKTFTVSST 187
Qy 205 LMLKVHKEDDGPVICOVEHFAVNTGLQRYLEQYKRPQVHIQMTYPLQGLTREGDAL 263
Db 188 LDFRVDSDDGVAVICRVHESLNATQVAMQVLEIHIYTPSVKI---IPSTPPPEGQPL 244
Qy 264 ELTCEAIKGPQPMVTVWVRVDDEN--PQHAVLSGNLFINNLTNDNGTYRCEASNIVGK 321
Db 245 ILTCESKGKLPPEPVLWKDGELPDPRVWVSGRELNLFLNKTNDNGTYRCEATNIGQ 304
Qy 322 AHSYMLYVYDPTTIPPPPTTTTTTTTTTTTTIIIT-DSRAGEEG 367
Db 305 SSAEYVLIVHDVNTLLFTIIPSLTTATVTVAITTSPTTSATTSIRDPNALAGQNG 364
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Qy 368 SIRAVDHAVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHAKGADDAADATTAIINA 427
Db 365 P----DHALIGGI VAVVVFVTLCSIFLLGRYLARHKGTYLNEAKGAEADAPDADTAIINA 420
Qy 428 EGGQNNSEKKEYFI 442
Db 421 EGSQVNAEKEKEYFI 435

Search completed: May 27, 2004, 09:34:55
Job time : 39.2466 secs
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DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
 Query Match 65.0%; Score 1483; DB 11; Length 295;
 Best Local Similarity 95.9%; Pred. No. 1.4e-118;
 Matches 283; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 QY 148 MIDIQKTAVEGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 207
 Db 1 MIDIQKTAVEGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 60
 QY 208 KVHKEDDGPVICOVEHPAVTGNLQRYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 267
 Db 61 KVHKEDDGPVICOVEHPAVTGNLQRYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIKGPQPMVTWVRVDEMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYM 327
 Db 121 EAIKGPQPMVTWVRVDEMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYI 180
 QY 328 LYVYDPTTIPPPPTTT 387
 Db 181 LYVYDPTTIPPPPTTT 240
 QY 388 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKKEYFI 442
 Db 241 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKKEYFI 295
 RESULT 13
 QYQYL5
 ID QYQYL5 PRELIMINARY; PRT; 289 AA.
 AC QYQYL5
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175B.
 GN IGSF4 OR RAI175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021965; BAA87915.1; -;
 DR MGD; MGI:1889272; IGSF4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D0565ABA4 CRC64;
 Query Match 61.1%; Score 1394; DB 11; Length 289;
 Best Local Similarity 91.9%; Pred. No. 5.6e-111;
 Matches 271; Conservative 3; Mismatches 15; Indels 6; Gaps 1;
 QY 148 MIDIQKTAVEGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 207
 Db 1 MIDIQKTAVEGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 60
 QY 208 KVHKEDDGPVICOVEHPAVTGNLQRYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 267
 Db 61 KVHKEDDGPVICOVEHPAVTGNLQRYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 120
 QY 268 EAIKGPQPMVTWVRVDEMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYM 327
 Db 121 EAIKGPQPMVTWVRVDEMPQHAVLSPNLFINNLTNDNGTYRCEASNIVGKAHSDYI 180
 QY 328 LYVYDPTTIPPPPTTT 387
 Db 181 LYVYDPTTIPPPPTTT 234
 QY 388 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKKEYFI 442
 Db 235 MLCLLIILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKKEYFI 289
 RESULT 14
 QYQYL3
 ID QYQYL3 PRELIMINARY; PRT; 278 AA.
 AC QYQYL3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175N.
 GN IGSF4 OR RAI175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urase K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RA175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021967; BAA87917.1; -;
 DR MGD; MGI:1889272; IGSF4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;
 Query Match 60.0%; Score 1370.5; DB 11; Length 278;
 Best Local Similarity 90.2%; Pred. No. 5.4e-109;
 Matches 266; Conservative 3; Mismatches 9; Indels 17; Gaps 1;
 QY 148 MIDIQKTAVEGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 207
 Db 1 MIDIQKTAVEGEIEVNCNTAMASKPATIRFWKGNTELKKGSEVEEWSMDYTVTSQML 60
 QY 208 KVHKEDDGPVICOVEHPAVTGNLQRYLEVQKPVQVHIQMTYPLQGLTREGDALELTC 267

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like protein 2.
 GN IGSF4 OR NECL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel cDNA encoding a member of immunosuperfamily.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF061260; AAC67243.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6F488 CRC64;

 Query Match 66.8%; Score 1526; DB 11; Length 295;
 Best Local Similarity 98.6%; Pred. No. 2.9e-122;
 Matches 291; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 148 MIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNTELKKGSEVEWSDMYTTSQML 207
 DB 1 MIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNTELKKGSEVEWSDMYTTSQML 60

 QY 208 KVHKEDGVPVICQVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTREGDALELTC 267
 DB 61 KVHKEDGVPVICQVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTREGDALELTC 120

 QY 268 EAIGKPOPVMVTVRVVDDEMPQHAVLSGNLFINLNKTDNGTYRCASNIVGAHSDYM 327
 DB 121 EAIGKPOPVMVTVRVVDDEMPQHAVLSGNLFINLNKTDNGTYRCASNIVGAHSDYM 180

 QY 328 LYVYDPTTTPPPPTTT 387
 DB 181 LYVYDPTTTPPPPTTT 240

 QY 388 MLCLLIIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNNSKEKEYFI 442
 DB 241 MLCLLIIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNNSKEKEYFI 295

 RESULT 11
 Q9QYL4
 ID Q9QYL4 PRELIMINARY; PRT; 306 AA.
 AC Q9QYL4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175C.
 GN IGSF4 OR RAI175C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";

RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021966; BAA87916.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;

 Query Match 65.9%; Score 1503.5; DB 11; Length 306;
 Best Local Similarity 94.8%; Pred. No. 2.5e-120;
 Matches 290; Conservative 2; Mismatches 3; Indels 11; Gaps 1;

 QY 148 MIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNTELKKGSEVEWSDMYTTSQML 207
 DB 1 MIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKGNTELKKGSEVEWSDMYTTSQML 60

 QY 208 KVHKEDGVPVICQVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTREGDALELTC 267
 DB 61 KVHKEDGVPVICQVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTREGDALELTC 120

 QY 268 EAIGKPOPVMVTVRVVDDEMPQHAVLSGNLFINLNKTDNGTYRCASNIVGAHSDYM 327
 DB 121 EAIGKPOPVMVTVRVVDDEMPQHAVLSGNLFINLNKTDNGTYRCASNIVGAHSDYM 180

 QY 328 LYVYDPTTTPPPPTTT 376
 DB 181 LYVYDPTTTPPPPTTT 240

 QY 377 IGVVAVVVFAMCLLIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNNSKE 436
 DB 241 IGVVAVVVFAMCLLIILGRYFARHKGTFTYTHEAKGADDAADATAIINAEQGNNSKE 300

 QY 437 KKEYFI 442
 DB 301 KKEYFI 306

 RESULT 12
 Q9QYL6
 ID Q9QYL6 PRELIMINARY; PRT; 295 AA.
 AC Q9QYL6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175A.
 GN IGSF4 OR RAI175A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Urabe K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021964; BAA87914.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.


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Db 61 TISCQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSLSNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTIIVLPPRNLMIDIOKDTAVEGEEIEVNCAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTIIVLPPRNLMIDIOKDTAVEGEEIEVNCAMASKPATIRWF 180
QY 181 KGNTELKGSSEVEESDMYTVTSQMLKVHKEDDGPVVICVEHPAVTGNLQRYLEVQ 240
Db 181 KGNTELKGSSEVEESDMYTVTSQMLKVHKEDDGPVVICVEHPAVTGNLQRYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVDDMPQHAVLSGNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTT-LTIIT 359
Db 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTTT-LTIIT 359
QY 360 DSRAGEGSIKAVDHAIGGVVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAAD 419
Db 361 DSRAGEGSIKAVDHAIGGVVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAAD 420
QY 420 ADTAIINAEQGNNSSEKKEYFI 442
Db 421 ADTAIINAEQGNNSSEKKEYFI 443

RESULT 6
Q7TNL1 PRELIMINARY; PRT; 417 AA.
AC Q7TNL1;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DE Nectin-like molecule 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
RT "Implications of nectin-like molecule
RT 2/IGSF4/RA175/SgIGSF/TS1C1/SynCAM1 in cell-cell adhesion and
RT transmembrane protein localization in epithelial cells.";
RL J. Biol. Chem. 0:0-0(2003).
DR EMBL; AY351388; AAQ02381.1; -
SQ SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;

Query Match 90.7%; Score 2071.5; DB 11; Length 417;
Best Local Similarity 91.7%; Pred. No. 9.2e-169;
Matches 408; Conservative 1; Mismatches 5; Indels 31; Gaps 2;

QY 1 MASVLPSSGSCAAA--AAAAAPGLRLRLRLLLLSAAALIPFGDGNLFTKDVTVIEG 57
Db 1 MASVLPSSGSCAAA--AAAAAPGLRLRLRLLLLSAAALIPFGDGNLFTKDVTVIEG 60
QY 58 EVATISQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSLSNVSIS 117
Db 61 EVATISQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSLSNVSIS 120
QY 118 DEGRYFCOLYTDPPQESYTIIVLPPRNLMIDIOKDTAVEGEEIEVNCAMASKPATI 177
Db 121 DEGRYFCOLYTDPPQESYTIIVLPPRNLMIDIOKDTAVEGEEIEVNCAMASKPATI 180
QY 178 RWFKGNTELKGSSEVEESDMYTVTSQMLKVHKEDDGPVVICVEHPAVTGNLQRYL 237
Db 181 RWFKGNTELKGSSEVEESDMYTVTSQMLKVHKEDDGPVVICVEHPAVTGNLQRYL 240
QY 238 EVQYKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVDDMPQHAVLSGN 297
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Db 241 EVQYKPVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVDDMPQHAVLSGN 300
QY 298 LFINLNKTDNGTYRCEASNIYVKAHSDYMLVYDPPPTTTPPTTTTTTTTTTILTI 357
Db 301 LFINLNKTDNGTYRCEASNIYVKAHSDYMLVY----- 334
QY 358 ITDSRAGEGSIKAVDHAIGGVVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDA 417
Db 335 --DSRAGEGSIKAVDHAIGGVVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDA 392
QY 418 ADADTAIINAEQGNNSSEKKEYFI 442
Db 393 ADADTAIINAEQGNNSSEKKEYFI 417

RESULT 7
Q86WB8 PRELIMINARY; PRT; 333 AA.
AC Q86WB8;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Secretory isoform of TSLC-1.
GN TSLC-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Ito A., Koma Y., Nagano T.;
RT "Cloning of a secretory isoform of SgIGSF/TS1C-1.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094146; BAC66178.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;

Query Match 75.1%; Score 1715; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 2.2e-138;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAA--AAAAAPGLRLRLRLLLLSAAALIPFGDGNLFTKDVTVIEG 60
Db 1 MASVLPSSGSCAAA--AAAAAPGLRLRLRLLLLSAAALIPFGDGNLFTKDVTVIEG 60
QY 61 TISCQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSLSNVSISDEG 120
Db 61 TISCQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLLNFSSELKVSLSNVSISDEG 120
QY 121 RYFCOLYTDPPQESYTIIVLPPRNLMIDIOKDTAVEGEEIEVNCAMASKPATIRWF 180
Db 121 RYFCOLYTDPPQESYTIIVLPPRNLMIDIOKDTAVEGEEIEVNCAMASKPATIRWF 180
QY 181 KGNTELKGSSEVEESDMYTVTSQMLKVHKEDDGPVVICVEHPAVTGNLQRYLEVQ 240
Db 181 KGNTELKGSSEVEESDMYTVTSQMLKVHKEDDGPVVICVEHPAVTGNLQRYLEVQ 240
QY 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVDDMPQHAVLSGNLFI 300
Db 241 YKQVHIQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVDDMPQHAVLSGNLFI 300
QY 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVY 331
Db 301 NNLNKTDNGTYRCEASNIYVKAHSDYMLVY 331
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Db 1 MASVLPSCGQCAAAVAAAAAAPPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 60
QY 58 EVATISCCQVKNKSDSVIQLLNPNTQTIYFRDPRPLKDSRFQLLNFSSSELKVSLLNVSTIS 117
Db 61 EVATISCCQVKNKSDSVIQLLNPNTQTIYFRDPRPLKDSRFQLLNFSSSELKVSLLNVSTIS 120
QY 118 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCCTAMASKPATI 177
Db 121 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCCTAMASKPATI 180
QY 178 RWFKNKTELKGSSEVEMSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLTQRYL 237
Db 181 RWFKNKTELKGSSEVEMSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLTQRYL 240
QY 238 EVQYKPVHIOQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVVDDEMPQHAVLSGN 297
Db 241 EVQYKPVHIOQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVVDDEMPQHAVLSGN 300
QY 298 LFINNINKTNGTYRCEASNIYGVKASDYMLYVYDPTTTPPTTTTTTTTTTTTTILTI 357
Db 301 LFINNINKTNGTYRCEASNIYGVKASDYMLYVYDPTTTPPTTTTTTTTTTTTTILTI 360
QY 358 ITDSRAGEEGSTRAVDHAGVIGVAVVAVFAMLCILIIILGRYFARHKGTYFTHKAGGADDA 417
Db 361 ITDSRAGEEGTIGAVDHAGVIGVAVVAVFAMLCILIIILGRYFARHKGTYFTHKAGGADDA 420
QY 418 ADADTAIINAEQQNNSEKKEYFI 442
Db 421 ADADTAIINAEQQNNSEKKEYFI 445

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RESULT 4

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Q8R5M8 ID Q8R5M8 PRELIMINARY; PRT; 456 AA.
AC Q8R5M8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAI175.
GN IGSF4 OR RAI175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Momoi T.;
RT "Biological function of RAI175, a new member of immunoglobulin super
RT family."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB064265; BAB8301.2; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 456 AA; 49787 MW; 3226E866A4BC1C7F CRC64;

```

Query Match 97.3%; Score 2221; DB 11; Length 456;
 Best Local Similarity 95.4%; Pred. No. 1.7e-181;
 Matches 435; Conservative 2; Mismatches 5; Indels 14; Gaps 2;

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QY 1 MASVLPSCGQCAAAVAAAAAAPPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 57
Db 1 MASVLPSCGQCAAAVAAAAAAPPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 60
QY 58 EVATISCCQVKNKSDSVIQLLNPNTQTIYFRDPRPLKDSRFQLLNFSSSELKVSLLNVSTIS 117
Db 61 EVATISCCQVKNKSDSVIQLLNPNTQTIYFRDPRPLKDSRFQLLNFSSSELKVSLLNVSTIS 120
QY 118 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCCTAMASKPATI 177
Db 121 DGRYFCQLYTDPPOESYTTIVLPPNLMIDIQKOTAVEGEEIEVNCCTAMASKPATI 180
QY 178 RWFKNKTELKGSSEVEMSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLTQRYL 237
Db 181 RWFKNKTELKGSSEVEMSDMYTTSQMLKVHKEDDGVVICQVEHPAVTGNLTQRYL 240
QY 238 EVQYKPVHIOQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVVDDEMPQHAVLSGN 297
Db 241 EVQYKPVHIOQMTYPLQGLTREGDALELTCEAIGKQPQVMVTVVVDDEMPQHAVLSGN 300
QY 298 LFINNINKTNGTYRCEASNIYGVKASDYMLYVYDPTTTPPTTTTTTTTTTTTTILTI 357
Db 301 LFINNINKTNGTYRCEASNIYGVKASDYMLYVYDPTTTPPTTTTTTTTTTTTTILTI 360
QY 358 ITDSRAGEEGSTRAVDHAGVIGVAVVAVFAMLCILIIILGRYFARHKGTY 406
Db 361 ITDSRAGEEGTIGAVDHAGVIGVAVVAVFAMLCILIIILGRYFARHKGTY 420
QY 407 FTHKAGGADDAADTAIINAEQQNNSEKKEYFI 442
Db 421 FTHKAGGADDAADTAIINAEQQNNSEKKEYFI 456

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RESULT 5

```

Q8N2F4 ID Q8N2F4 PRELIMINARY; PRT; 443 AA.
AC Q8N2F4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein HEMBA1001879.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Makamatsu A., Nagai T., Nakamura Y.,
RA Nagahara K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BAC11657.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IGC2; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;

```

Query Match 93.5%; Score 2134.5; DB 4; Length 443;
 Best Local Similarity 94.4%; Pred. No. 4.1e-174;
 Matches 418; Conservative 4; Mismatches 20; Indels 1; Gaps 1;

```

QY 1 MASVLPSCGQCAAAVAAAAAAPPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 60
Db 1 MASVLPSCGQCAAAVAAAAAAPPGLRLRLRLLSAAALPTGQGNLFTKQVTVIEG 60
QY 61 TISCCQVKNKSDSVIQLLNPNTQTIYFRDPRPLKDSRFQLLNFSSSELKVSLLNVSTIS 120

```

QY 61 TISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSSELKVSILTNVSI 120
 Db 61 TISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSSELKVSILTNVSI 120
 QY 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDTAVEGEEIEVNCCTAMASKPAT 180
 Db 121 RYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDTAVEGEEIEVNCCTAMASKPAT 180
 QY 181 KGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYL 240
 Db 181 KGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYL 240
 QY 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVMVTVWRVDEMPQHAVL 300
 Db 241 YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVMVTVWRVDEMPQHAVL 300
 QY 301 NNLNKTNGTYRCEASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTIT 360
 Db 301 NNLNKTNGTYRCEASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTIT 360
 QY 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 420
 Db 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 420
 QY 421 DTALINAEAGGNNSEKKEYFI 442
 Db 421 DTALINAEAGGNNSEKKEYFI 442

RESULT 2

Q8R41L ID Q8R41L PRELIMINARY; PRT; 445 AA.
 AC Q8R41L;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tumor suppressor in lung cancer 1.
 GN IGSF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RA Fukami T., Maruyama T., Murakami Y.;
 RT "Identification of murine orthologue of the TSLC1 gene."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF434663; AAL86736.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003585; Neurexin-like.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;

Query Match 98.2%; Score 2241.5; DB 11; Length 445;
 Best Local Similarity 98.0%; Pred. No. 2.8e-183;
 Matches 436; Conservative 1; Mismatches 5; Indels 3; Gaps 1;

QY 1 MASVLPVPSGSCAAA---AAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEG 57
 Db 1 MASVLPVPSGSCAAA---AAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEG 60

QY 58 EVATISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSSELKVSILTNVSI 117
 Db 61 EVATISQVKNKSDSVIQLLNPNRQTIYFRDRLKDSRFQLLNFSSSELKVSILTNVSI 120
 QY 1-8 DEGRYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDTAVEGEEIEVNCCTAMASKPAT 177
 Db 121 DEGRYFCOLYTDPPQESYTTITVLVPPRNLMIDIKDTAVEGEEIEVNCCTAMASKPAT 180
 QY 178 RWFKGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYL 237
 Db 181 RWFKGNTELKSGSEVEWSDMYTTSQMLKVKHEDDGPVICOVEHPAVTGNLQTOXYL 240
 QY 238 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVMVTVWRVDEMPQHAVL 297
 Db 241 EVOYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPOQVMVTVWRVDEMPQHAVL 300
 QY 298 LFNNLNKTNGTYRCEASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTIT 357
 Db 301 LFNNLNKTNGTYRCEASNVGKAHSDYMLVYVDPPTTTPPTTTTTTTTTTTTTIT 360
 QY 358 ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 417
 Db 361 ITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMCLLIILGRYFAHKGTYFTHEAKGADDA 420
 QY 418 ADADTAIINAEAGGNNSEKKEYFI 442
 Db 421 ADADTAIINAEAGGNNSEKKEYFI 445

RESULT 3

Q8K3T6 ID Q8K3T6 PRELIMINARY; PRT; 445 AA.
 AC Q8K3T6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Synaptic cell adhesion molecule 1.
 GN IGSF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Biederer T., Sara Y., Moshayeva M., Atasoy D., Liu X., Kavalali E.T.,
 RA Sudhof T.C.;
 RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly."
 RL Science 0:0-0(2002).
 DR EMBL; AF539424; AAN01614.1; -.
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR GO; GO:0007416; P:synaptogenesis; IDA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00409; IGC2; 3.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match 97.8%; Score 2232.5; DB 11; Length 445;
 Best Local Similarity 97.5%; Pred. No. 1.7e-182;
 Matches 434; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

QY 1 MASVLPVPSGSCAAA---AAAAAPPGLRLRLRLLLLSAAALIFTGQGNLFTKDVTVIEG 57

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 36.2466 Seconds
(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187b-2

Perfect score: 283

Sequence: 1 MASVLPSSGSCAAAAA.....AIIAEGGQNNSEKKEYFI 442

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2280	99.9	442	Q9BY67	Q9BY67 homo sapien
2	2241.5	98.2	445	11 Q8R4L1	Q8R4L1 mus musculus
3	2232.5	97.8	445	11 Q8K3T6	Q8K3T6 mus musculus
4	2221	97.3	456	11 Q8R5M8	Q8R5M8 mus musculus
5	2134.5	93.5	443	4 Q8N2P4	Q8N2P4 homo sapien
6	2071.5	90.7	417	11 Q7TNL1	Q7TNL1 mus musculus
7	1715	75.1	333	4 Q86WB8	Q86WB8 homo sapien
8	1683.5	73.7	336	11 Q8OVG4	Q8OVG4 mus musculus
9	1671.5	73.2	336	11 Q9D6E7	Q9D6E7 mus musculus
10	1526	66.8	295	11 Q922H8	Q922H8 mus musculus
11	1503.5	65.9	306	11 Q9QYL4	Q9QYL4 mus musculus
12	1483	65.0	285	11 Q9QYL6	Q9QYL6 mus musculus
13	1394	61.1	289	11 Q9QYL5	Q9QYL5 mus musculus
14	1370.5	60.0	278	11 Q9QYL3	Q9QYL3 mus musculus
15	903	39.6	435	4 Q8N3J6	Q8N3J6 homo sapien
16	893	39.1	437	4 Q81ZP8	Q81ZP8 homo sapien

17	863	37.8	395	11	Q8BXJ7	Q8BXJ7 mus musculus
18	862.5	37.8	404	11	Q8BLQ9	Q8BLQ9 mus musculus
19	860	37.7	395	11	Q8BZP4	Q8BZP4 mus musculus
20	858.5	37.6	404	11	Q8BYF1	Q8BYF1 mus musculus
21	802	35.1	394	13	Q7ZXX1	Q7ZXX1 xenopus lae
22	767	33.6	388	4	Q8NFZ8	Q8NFZ8 homo sapien
23	758	33.2	388	11	Q8R464	Q8R464 mus musculus
24	744.5	32.6	396	11	Q9NM28	Q9NM28 mus musculus
25	739	32.4	398	4	Q8N126	Q8N126 homo sapien
26	732.5	32.1	381	4	Q9Y4A4	Q9Y4A4 homo sapien
27	722	31.6	432	4	Q9UJL1	Q9UJL1 homo sapien
28	379.5	16.6	163	11	Q8K1H8	Q8K1H8 mus musculus
29	370.5	16.2	163	4	Q9NVJ5	Q9NVJ5 homo sapien
30	368.5	16.1	152	11	Q8BSQ8	Q8BSQ8 mus musculus
31	341.5	15.0	549	11	Q9D006	Q9D006 mus musculus
32	338.5	14.8	549	11	Q9JLB9	Q9JLB9 mus musculus
33	335.5	14.7	549	4	Q9NQ83	Q9NQ83 homo sapien
34	325.5	14.3	234	4	Q81ZQ9	Q81ZQ9 homo sapien
35	315.5	13.9	438	11	Q9JLB7	Q9JLB7 mus musculus
36	315.5	13.9	510	11	Q9JLB8	Q9JLB8 mus musculus
37	287	12.6	439	13	Q57349	Q57349 gallus gall
38	268	11.7	407	4	Q9Y412	Q9Y412 homo sapien
39	265	11.6	1482	5	Q9V4Y0	Q9V4Y0 drosophila
40	263.5	11.5	5175	5	Q810L3	Q810L3 caenorhabdi
41	261.5	11.5	5198	5	Q76518	Q76518 caenorhabdi
42	261.5	11.5	510	4	Q96N18	Q96N18 homo sapien
43	261.5	11.5	510	4	Q96K15	Q96K15 homo sapien
44	254.5	11.1	400	6	Q8HY16	Q8HY16 cebus apell
45	247.5	10.8	530	11	Q80XJ5	Q80XJ5 mus musculus

ALIGNMENTS

RESULT 1

Q9BY67 Q9BY67 PRELIMINARY; PRT; 442 AA.
AC Q9BY67;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Nectin-like protein 2.
GN NECL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin superfamily.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132811; AAF69029.1; -.
DR Genbank; HGNC:5951; IGSP4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurxin-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 99.9%; Score 2280; DB 4; Length 442;

Best Local Similarity 99.8%; Pred. No. 1.4e-186;

Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPGTGQNLFTKDVTVIEGEVA 60

DB 1 MASVLPSSGSCAAAAAAPPGLRLRLLLLFSAALIPGTGQNLFTKDVTVIEGEVA 60


```

FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 698 718 POTENTIAL.
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT CHAIN 21 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 837 AA; 92932 MW; C3D034106C5741C1 CRC64;

Query Match 9.7%; Score 222; DB 1; Length 837;
Best Local Similarity 24.1%; Pred. No. 2.6e-08;
Matches 120; Conservative 70; Mismatches 172; Indels 136; Gaps 28;

Qy 49 TKDVTVI-----BGEVATISQVKNKSDSDVQLINPRTQTYPRDF 89
Db 102 TQETAVLEIYQKLTREWSQBFKQGDAAVVCVRSSPAPAVSLYHNEEV----- 155
Qy 90 RPLKDSFOLINSSSELKSLTWSIDSGRYFCOLYDTPQF-SYTTIVL--VPRN 146
Db 156 TTISDNLAML-----ANNLOILNINKSDGIYRCEGRVARGIDRDIIVNVVPAI 211
Qy 147 LMIDIQKD---TAVEGEIEVNCATAMSKPATTIRWFKGNTLKGSEVSEWSDMYTV-- 201
Db 212 SM--POKSFNATABRGEMTFSCRASGS-PPPAISWFR-----NGKL-IEE-NEKYILKG 261
Qy 202 -TSQMLKVKHKEDGVPIQVEHPATGNLOTORYLEVQVQKPVHIOHTYPLQGLTREG 260
Db 262 SNELTVRNINSGGYVCRATNKA--GEDEKQAFQVFPQPHI-IQLK---NETTYEN 315
Qy 261 DALELTCEAIGKPOPMVTWVR-VD-----DMP-----QHAVLSQPNLFINNLN 304
Db 316 GQVTLVCDAGEPIP-BITWKRAVDGFTFTGDKSPGRIEVKGQH---GSSSLHIKDVK 371
Qy 305 KTDNGTYRCE-ASNIVGKAHSDYMLYVY-----DPPPTT 336
Db 372 LSGSGRYDCEAASRIGGHOKSMYLDIEYAPKFSNQTIYYSWEGNPINISCDVKSNPPAS 431
Qy 337 I-----PPPTTTTTTTTTTTTTTTTTLITDSRAGEG--SIRAVDHAVIGGVAVVV 395
Db 432 IHWERDKVLVPAKNTNMLKYSTGRKMLEIAPSDNDGFRYCNCTATNH--IGTRFQEI 489
Qy 386 FAMLCL-----LIILGRYFAR-----HKGTYFTHEAKGADDAADATTAI NAEG 429
Db 490 LALADVPSSPYGVKILIELSQTAKVSNKPDSDHGGVPIHHYQVDVKEVASEIWKIVRSHG 549
Qy 430 GQ-----NNSEEKKEYFI 442
Db 550 VQTMVVLNNLEPNTTVEI 567

```

RESULT 15

NPHN MOUSE
 ID NPHN_MOUSE STANDARD; PRT; 1242 AA.
 AC Q9QZS7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
 Nephtrin precursor (renal glomerulus-specific cell adhesion receptor).
 NPHS1 OR NPHN.
 Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 RX MEDLINE=99436348; PubMed=10504499;
 RA Holzman L.B., St John P.L., Kovazi I.A., Verma R., Holthofer H.,
 RA Abrahamson D.R.;
 RT "Nephtrin localizes to the slit pore of the glomerular epithelial
 cell";
 RL Kidney Int. 56:1481-1491(1999).
 [2]
 RP INTERACTION WITH CD2AP.
 RX MEDLINE=21590051; PubMed=11733379;
 RA Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
 RA "CD2AP localizes to the slit diaphragm and binds to nephrin via a
 novel C-terminal domain";
 RL Am. J. Pathol. 159:2303-2308(2001).
 [3]
 RP INTERACTION WITH CD2AP AND NPHS2.
 RX MEDLINE=21590460; PubMed=11733557;
 RA Schwarz K., Simons M., Reiser J., Saleem M.A., Paul C., Kriz W.,
 RA Shaw A.S., Holzman L.B., Mundel P.;
 RT "Podocin, a raft-associated component of the glomerular slit
 diaphragm, interacts with CD2AP and nephrin";
 RL J. Clin. Invest. 108:1621-1629(2001).
 CC -!- FUNCTION: Seems to play a role in the development or function of
 the kidney glomerular filtration barrier. May anchor the podocyte
 slit diaphragm to the actin cytoskeleton.
 CC -!- SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
 domain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Located
 at podocyte slit diaphragm between podocyte foot processes.
 CC -!- TISSUE SPECIFICITY: Expressed in kidney glomeruli.
 CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -!- SIMILARITY: Contains 8 immunoglobulin-like domains.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; AF168466; AAF03368.1; --
 CC MGD; MGI:1859637; Nphs1.
 CC GO; GO:0005515; F:protein binding; IPT.
 CC GO; GO:0007254; P:JNK cascade; IDA.
 CC GO; GO:000165; P:MAPKK cascade; IDA.
 CC InterPro; IPR008957; FN III-like.
 CC InterPro; IPR003961; FN-III.
 CC InterPro; IPR007110; IG-like.
 CC Pfam; PF00041; fn3; 1.
 CC Pfam; PF00047; ig; 8.
 CC SMART; SM00060; FN3; 1.
 CC SMART; SM00408; IGC2; 1.
 CC PROSITE; PS50835; IG_LIKE; 8.
 CC Cell adhesion; Transmembrane; Signal; Glycoprotein;
 CC Immunoglobulin domain; Repeat; Phosphorylation.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 1242 NEPHRIN.
 FT DOMAIN 23 1064 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1065 1086 POTENTIAL.
 FT DOMAIN 1087 1242 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 1330 IG-LIKE C2-TYPE 1.

CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M76710; AAA49910.1; -.
DR PIR; JN0635; JN0635.
DR HSP; P56276; ITLK.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN-III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; IG-LIKE; 5.
DR Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1092
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1092
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 208 295
FT DOMAIN 303 397
FT DOMAIN 400 489
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118082 MW; CD336E0F8B7AD1 CRC64;
Query Match 9.8%; Score 223; DB 1; Length 1092;
Best Local Similarity 24.2%; Pred. No. 3.1e-08;
Matches 82; Conservative 67; Mismatches 150; Indels 40; Gaps 15;
QY 50 KDVTVIRGEVATISC---QVKS---DDSVIQLN-----PNQTIYPRDPRPKDSRFOL 99
DB 199 KDQIVNVPLQARQIRVNATNMDSVLSCDADGFPDPEISWLKKGIEDGE-EK 257
QY 100 LNFSSSLKSLNIVSISDGRFYFCOLYTPPOBSYTIIVLPNMLMDIQKDTAVEG 159
DB 258 ISNEDKSEMTIVVEKEDAEVSC-IANNQAGEAEAILVKYAKPKMYVENKUTVEL 316
QY 160 EELEVNCTAMASKPATIRIRFKNGTELKSGSEVEESDMYTVT-----SOLMLKVHKED 213
DB 317 DEITLTCEA-SGDPIPSITW---RTAHRNISSEKTLGDGHVVKDHRMSALTLDKIQYT 372
QY 214 DGVFVLCQVEHPAVTGNLQRYLEQVQKPVHQMITYPQGLTREGDALELTCEAIGKP 273
DB 373 DAGEYFCVASNP-IGVDMQAM-YFEVQYAPKIR---GPVVVYTWEGNPNVITCDVLAPH 426

QY 274 QPVMVTVRVDDDEMPQH-----AVLSGP---NLFINNINKTNGTYRCASNVGKAHSD 325
DB 427 S-AVNSWFRDGGQLPSSNFSNFKIYNGPTFSLELVNPDSENFNGYNCSAVNSIGHESE 485
QY 326 YMLYVYDPTTTPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 364
DB 486 FILVQADTSS---PAIRKVEPYSTVMIVFDEPDATGG 521
RESULT 14
NCM2_HUMAN
ID NCM2_HUMAN STANDARD; PRT; 837 AA.
AC O15394;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN NCM2 OR NCAM21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369930; PubMed=9226371;
RA Paeloni-Giacobino A., Chen H., Antonarakis S.E.;
RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
RT that maps to chromosome region 21q21 and is potentially involved in
RT Down syndrome.";
RL Genomics 43:43-51 (1997).
RN [2]
RP CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666 (2003).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC brain.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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CC
CC EMBL; U75330; AAB80803.1; -.
DR Genew; HGNC:7657; NCAM2.
DR MIM; 602040; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0007158; P:neuronal cell adhesion; TAS.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN-III.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG-LIKE; 5.
DR Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT POTENTIAL.


```
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 GPI-anchor amidated asparagine
FT LIPID (Potential).
FT SEQUENCE 344 AA; 37998 MW; CBB39BE5B33B224 CRC64;
Query Match 10.1%; Score 230; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 2.2e-09;
Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;
QY 29 LLLLSAALIPFGDQGNLFK---DVTVEGEVATISQVKNKSDSDSVIQLLNPRTI- 84
Db 19 LRLLELVPTGVPRSGDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAMLNRSSTIL 75
QY 85 YFRDFRPLKDSRFQLLNFSSSELKSLVNTNVSISDEGRYFCQLYTD-PPQESYTTITVLVP 143
Db 76 YAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVS 135
QY 144 PRNLMIDIOKDTAV-EGEIEVNTCTAMASKPATIRFWKGNTELKKGSEVEESDMYTVT 202
Db 136 PK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTVRHHISPKAVGFVSEDEYLEIQGIT 192
QY 203 SOLMLKVH---KEDDGPVVICQVEHPAVTGNLQRTQRYLEVQYKPVQVHIQMTYPLQGL-TR 258
Db 193 REOSGEYECASNDVAAPVRRV---VTNYPPIYS-----EAKGTGVP 234
QY 259 EGDALLETCEALGKQPPQVMTVTRVDDDEMPQ-----HVLSGNLFNINLNKTNDG 309
Db 235 VGQKGTLOCEASAVPS-AEFQWFKDKRLIEGKGVKVENRPFSLRLTFP--NVSEHDYG 291
QY 310 TYRCEASNVGKAHSDYMLY 329
Db 292 NYTCVASNKLGHNTASIMLF 311
RESULT 11
NTRI_HUMAN
ID NTRI_HUMAN STANDARD; PRT; 344 AA.
AC Q9P121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (hnt).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT "Cloning and identification of human neurotrophin full length cDNA.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLN
family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF126426; AAF37591.1; -.
DR MIM; 607938; -.
DR GO; GO:0008038; P:neuronal cell recognition; TAS.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 321 NEUTROTRIMIN.
FT PROPEP 322 344 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 126 IG-LIKE C2-TYPE 1.
FT DOMAIN 136 218 IG-LIKE C2-TYPE 2.
FT DOMAIN 222 309 IG-LIKE C2-TYPE 3.
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 321 321 GPI-anchor amidated asparagine
FT SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;
Query Match 10.0%; Score 228; DB 1; Length 344;
Best Local Similarity 26.4%; Pred. No. 3.1e-09;
Matches 84; Conservative 54; Mismatches 138; Indels 42; Gaps 14;
QY 29 LLLLSAALIPFGDQGNLFK---DVTVEGEVATISQVKNKSDSDSVIQLLNPRTI- 84
Db 19 LRLLELVPTGVPRSGDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAMLNRSSTIL 75
QY 85 YFRDFRPLKDSRFQLLNFSSSELKSLVNTNVSISDEGRYFCQLYTD-PPQESYTTITVLVP 143
Db 76 YAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVS 135
QY 144 PRNLMIDIOKDTAV-EGEIEVNTCTAMASKPATIRFWKGNTELKKGSEVEESDMYTVT 202
Db 136 PK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTVRHHISPKAVGFVSEDEYLEIQGIT 192
QY 203 SOLMLKVH---KEDDGPVVICQVEHPAVTGNLQRTQRYLEVQYKPVQVHIQMTYPLQGL-TR 258
Db 193 REOSGEYECASNDVAAPVRRV---VTNYPPIYS-----EAKGTGVP 234
QY 259 EGDALLETCEALGKQPPQVMTVTRVDDDEMPQ-----HVLSGNLFNINLNKTNDGTY 311
Db 235 VGQKGTLOCEASAVPS-AEFQWFKDKRLIEGKGVKVENRPFSLRLTFP--NVSEHDYG 293
QY 312 RCEASNVGKAHSDYMLY 329
Db 294 TCVASNKLGHNTASIMLF 311
RESULT 12
NCM2_MOUSE
ID NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=3ALB/c; TISSUE=Olfactory neuroepithelium;
```

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences."
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Neural cell adhesion molecule.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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CC EMBL; AF282980; AAK00276.1; -;
 CC EMBL; BC023307; AAH23307.1; -;
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003599; IG.
 CC InterPro; IPR003598; IG_c2.
 CC Pfam; PF00047; IG; 3.
 CC SMART; SM00409; IG; 3.
 CC SMART; SM00408; IGC2; 3.
 CC PROSITE; PS50835; IG-LIKE; 3.
 CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 KW Repeat; Signal; Lipoprotein.

FT SIGNAL 1 31
 FT CHAIN 32 321
 FT PROPEP 322 344
 FT DOMAIN 39 126
 FT DOMAIN 136 218
 FT DOMAIN 222 309
 FT DISULFID 57 115
 FT DISULFID 157 201
 FT DISULFID 243 295
 FT CARBOHYD 44 44
 FT CARBOHYD 70 70
 FT CARBOHYD 152 152
 FT CARBOHYD 284 284
 FT CARBOHYD 292 292
 FT CARBOHYD 305 305
 FT CARBOHYD 321 321
 FT CARBOHYD 321 321
 FT LIPID 321 321
 FT CONFLICT 75 75
 FT CONFLICT 92 92
 FT CONFLICT 119 119
 FT CONFLICT 187 187
 FT CONFLICT 213 213
 FT CONFLICT 225 225
 FT SEQUENCE 344 AA; C885BBA52C148554 CRC64;

Query Match 10.1%; Score 231; DB 1; Length 344;

Best Local Similarity 26.2%; Pred. No. 1.9e-09;

Matches 84; Conservative 54; Mismatches 136; Indels 46; Gaps 14;

29 LLLFSAALIPGTGQNLFTK---DVTVEGEVATISQWNSKSDSDSVIQLLNPRTI- 84

19 LRLFLVPTGVPVRSGDATEPKAMDNVTVRQGESATLRCTI---DNRTVAVMLNSTIL 75

85 YFDFRPLKDSRQLLNFSSSELKVSILTNVSDIGRYFQLTYD-PPQSYTTITVLVP 143

76 YAGDKWCLDPVRLVLSNTQTSIEIQNVDDVDEGPTCVQTDNHPKTSRVHLIVQVS 135

144 PRLMIDIQKDTAV-EGEEIEVNCVTAMASKPATITRMFKNTKELKGEVSEWSDMTVT 202

136 PK--IVEISSDISGNNISLTCIA-TGRPEPTVTRHISPKAVGVSEDEYLEIQGIT 192

203 SQLMKLVH---KEDDGVPVTCQVEHPAVTGNLTQRYLEYQYKPVQHIQMTYPLQGL-TR 258

Db 193 REOSGEYCSASNDVAAPVVRVK-----VTNYPPIYS-----EAKGTGVP 234
 Qy 259 EGDALLETCEAIKGPQPMVTVVRVDEMPQ-----HAVLSGNLFINNKNTNG 309
 Db 235 VGQKGTQLQCSASAVPS-AEPQWFRKDKRLVGGKGVKVENRPFSLKLTFF--NVSEHDYG 291
 Qy 3-0 TYRCEASNIYVKAHSDYMLY 329
 Db 292 NYTCVASNKLGHNTASIMLF 311

RESULT 10

NTRI RAT

ID NTRI RAT STANDARD; PRT; 344 AA.

AC Q62718;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neurotrophin precursor (GF65).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.

RC STRAIN=Sprague-Dawley;

RC MEDLINE=95198094; PubMed=7891157;

RA Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,

RA Salzer J.L.;

RA "Cloning of neurotrophin defines a new subfamily of differentially

RT expressed neural cell adhesion molecules.";

RL J. Neurosci. 15:2141-2156 (1995).

CC -!- FUNCTION: Neural cell adhesion molecule.

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: Central nervous system.

CC -!- DEVELOPMENTAL STAGE: Expressed at high levels in several

CC developing projection systems: in neurons of the thalamus,

CC subplate, and lower cortical laminae in the forebrain and in the

CC portine nucleus, cerebellar granule cells, and Purkinje cells in

CC the hindbrain.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON

CC family.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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CC EMBL; U16845; AAA67445.1; -;

DR PIR; I56551; I56551.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; IG; 3.

DR SMART; SM00408; IGC2; 2.

DR PROSITE; PS50835; IG-LIKE; 3.

DR Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;

KW Repeat; Signal; Lipoprotein.

FT SIGNAL 1 31

FT CHAIN 32 321

FT PROPEP 322 344

FT DOMAIN 39 126

FT DOMAIN 136 218

FT DOMAIN 222 309

FT DISULFID 57 115

FT DISULFID 157 201

FT DISULFID 243 295

FT CARBOHYD 44 44

FT CARBOHYD 70 70

FT CARBOHYD 152 152

POTENTIAL.

NEUROTROPHIN.

REMOVED IN MATURE FORM (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

DR PIR: B44194; B44194.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 3.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 85 85
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT CARBOHYD 386 392
 FT VARSPLIC
 FT VARSPLIC 393 417
 FT SEQUENCE 417 AA; 45464 MW; DA4AD0F4D2F6E1F CRC64;
 Query Match 10.7%; Score 244; DB 1; Length 417;
 Best Local Similarity 23.5%; Pred. No. 2.8e-10;
 Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;
 QY 13 AAAAAAAPPGLRLRLLLLFSAALPTGCGQNLFTKQVTV--IGEVATISC--QVVK 68
 Db 2 ARTMAAAPP-----LLTLLELSWPPPGTGDIIVQAQTPQVGLGSDVTPCYLQVPG 55
 QY 69 SDDSVIQLLNPNR-----QTIYFRDFRPLKDSRFQLLNFSSELKSLVLTNVS-----I 116
 Db 56 MEETHVSQLTWSRHGSGSMVAFHQYGNYSFEPKLEFVAARLGTLDASLUMGLRV 115
 QY 117 SDEGRFYCOLYDPPQESYTT---ITVLPPNLMIDIQDTAVEGEEIEV-NCTAMASK 172
 Db 116 EDEGNYTC-LFVTFPGQSRSDIWLRLAKPN-TAEVQK-VQLTGKPPVAVRCVSTGCR 172
 QY 173 PATTIRWFKGNTLKGSEVEE-----WSDMYTVTSQMLKVHKEDDGVPIQVHEHPAVT 228
 Db 173 PPAHITW---HSLDGMNPTSQAQFLSTGTVTITSLWILVPSQVDGKSVTCCKVEHESPE 229
 QY 229 GNLOFQVLYEQKPVHIONTYPLQGLTREGDALELTCEALGKQPVMVTVRVVDENP 288
 Db 230 KPQLLTALVNTVYPPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNEPPTGYNNSTWTGGLP 287
 QY 299 QHVLVSGNLFNNLNKTDNGYRCEASNIYKSHSDYMLYVDPPTPIPTPTTTTTTTTT 348
 Db 288 PFVAQGAQLLRPVDKPINTTFICNVNTALGARQALTVQKGGPPSPFGSMSSN---- 343
 QY 349 TTTTITLTITDSRAGEEGSIRAVDHVIGGVVAVVVFAMLLCLLIL-----GRYFAHK 403
 Db 344 -----IIIFLILGIVILLTLGLGIVGYFYRSR 369
 QY 404 GT-----YPTHEAKGADDAADATAIINAEAGGQNNSEKKE 439
 Db 370 CSREPLWCHLSPSSEEHASA-----SANGYISYSDVSRE 404
 RESULT 5
 PVR2_HUMAN
 ID PVR2_HUMAN STANDARD; PRT; 538 AA.
 AC Q92692; O75485; Q96329;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
 mediator B) (HvEB) (Nectin 2) (CD112 antigen).
 GN PVRL2 OR PRR2 OR HVEB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95347610; PubMed=7622062;
 RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
 RA "The human PRR2 gene, related to the human poliovirus receptor gene
 (PVR), is the true homolog of the murine MPH gene.";
 RL Gene 159:267-272(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=98321161; PubMed=9657005;
 RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
 RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
 RA "A cell surface protein with herpesvirus entry activity (HvEB) confers
 susceptibility to infection by mutants of herpes simplex virus type
 1, herpes simplex virus type 2, and pseudorabies virus.";
 RL Virology 246:179-189(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting J., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 31-538 FROM N.A.
 RA Yoshiura K., Murray J.C.;
 RT "A transcriptional map in the region of 19ql3 derived using direct
 sequencing and exon trapping";
 RL Submitted (JAN-1998) to the ENBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 449-538 FROM N.A.
 RX MEDLINE=99449047; PubMed=10520737;
 RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
 RA Ashworth L.K., Van Bockmeier F.M., Dawkins R.L.;
 RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
 PEREC1";
 RL DNA Seq. 9:89-101(1998).
 CC -!- FUNCTION: RECEPTOR FOR ALPHAPERSESVIRUS (HSV-1, HSV-2 AND
 CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Delta;
 CC IsoId=Q92692-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;

```

RL J. Virol. 73:4493-4497(1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAPERPVIRUS (SUCH AS MURINE HSV) ENTRY
CC INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC -----
CC EMBL; M80206; AAA39734.1; -.
CC EMBL; D26107; BAA05103.1; -.
CC EMBL; BC059941; AAB59941.1; -.
CC PIR; A38211; HLMSP3.
CC PIR; A53437; A53437.
CC MGD; MGI:97822; Pvr12.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00406; IgV; 1.
CC PROSITE; PS50835; IG_LIKE; 3.
CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
CC Repeat; Alternative splicing.
CC SIGNAL 1 31 POTENTIAL.
CC CHAIN 32 530 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
CC DOMAIN 32 351 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 352 372 POTENTIAL.
CC DOMAIN 373 530 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 32 147 IG-LIKE V-TYPE.
CC DOMAIN 153 247 IG-LIKE C2-TYPE 1.
CC DOMAIN 252 337 IG-LIKE C2-TYPE 2.
CC DISULFID 54 131 BY SIMILARITY.
CC DISULFID 174 229 BY SIMILARITY.
CC DISULFID 274 320 BY SIMILARITY.
CC CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
CC VARSPIC 339 467 ESPSTAGATGGTGGIIGGIIAIIATVAGTGILICROORKE
CC ORLOADEEELEGGPSKPTPKAKLEPEEMPSQLFTLGA
CC SEHSPTVPYFDAGVSCADQEMPRYHELPTEERSGPLLIG
CC ATGLGP -> DTPQASRDVGLVWAVGVTLLVLLAGGL
CC ALILLGRRRKSPGGGNDGSDYDPKTVQFGNGPWFV
CC RSASPEMRDPCDEDEEEMKAEEGLMPPHESPRDPM
CC ESHLDGSLISRRVYV (in isoform Alpha).
CC /FtId=VSP_002630.
CC Missing (in isoform Alpha).
CC /FtId=VSP_002631.
CC VARSPIC 468 530
CC SEQUENCE 530 AA; 57317 MW; 0ED71BFA2B231BBE CRC64;
CC
CC Query Match
CC Best Local Similarity 10.8%; Score 247.5; DB 1; Length 530;
CC Matches 91; Conservative 63; Mismatches 166; Indels 91; Gaps 14;
CC
CC 15 AAAAAPP-----LRRLRLLLFSAALPTGSGQLTKVTYVIGEV---ATISQCV 66
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 2 ARAAVLPPSLRSTPLPLPILL-----LQETGAQDVRVRVPEVGRGLGGTVLFCFL 56
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 67 -----NKGDSVYQLLNPNTQYIFRDFRPLKDSRFQL-----LNFSSS 105
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CC 57 LPPTTERRVSQVWQRLDGTVAAPHPG-----FGVDPSNQSFKDRLSFVRARPETNADLR 112
CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 106 ELKSLTNVTSISDEGRYFCQLYTD--POESYTTITVLVPPRNLMIDIQDQTAVEGEIE 163
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 113 DATLAFRLGRVDEGNTCEPATFNGTRRGVTLWRVIAQEN-----HAAQAEVT 163
QY 154 V-----NCTAMASKPATIRFKG-NTELKGSVEEMSDMYTVTSQMLKVKHEDD 214
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 IGQSVAVARCVSTGGRPPARITWISSLGGAKDTQFGIOAGVTVTIISRYSLVPVGRAD 223
QY 215 GVPVICQVEHPANTGNIQTORYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 224 GVKVTCRVEHSEFEPILLPVTLSRVYPPEVIS-GYDDNNWYLGSEAI-LTCDVRNPE 281
QY 275 PVMYTVRVVDEMPQHAVLSPNLFNNLNKNTGTYRCASNIVGKAHSDYMYLVYDDPP 334
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 282 PTYDWMSTTSGVFPASAVAQSQSLVHSVDRMVTTFICTATNAVGTGRAEQVILVRESP 341
QY 335 TTIPPTPTTTTTTTTTTTTTTTTITDSTRAGEEGSIRAVDHAVIGVVAVV 385
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 342 ST-----AGAGATGGI-----IGGIATAII 361

RESULT 4
PVR_CERAE
ID -PVR CERAE STANDARD; PRT; 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RS SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059651; PubMed=1331508;
RA Koike S., Ise Y., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain.";
RL J. Virol. 66:7059-7066(1992);
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP_002622, VSP_002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC -----
CC EMBL; D12611; BAA02136.1; -.
CC EMBL; D12612; BAA02137.1; -.
CC PIR; A44194; A44194.

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QY 297 NLFNN--LNKTDNTGTYRCEASNIWGAHSDYMLVYPDPPTTPPPTTTTTTTTTTTIL 355
Dd 298 : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Dd 299 TLFFKGFINSLAGTYICEATNPITSGVGQVENNITEFPTYPSPE----- 344
Qy 356 TIITDSRAGEGSRAVDHAVIGGVAVVFMMCLLIILGRYA----RH--KGTFT- 408
Dd 345 ---HGRRAG---PVPFAIIGCVAGSI---LLVLIVGGVVVALRRRTFKGDYSTK 392
Qy 409 -----HEAKGA-----DDAADADTAINAEGGNSEEKE 439
Dd 393 KHYVNGYSKAGIPQHHPPAQNLOYPDSDDEKA---GLPGSSYYEEEEE 442

RESULT 3

PVR2 MOUSE	ID_PVR2_MOUSE	STANDARD;	PRT;	530 AA.
AC	P32507; Q62096;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Poliovirus receptor related protein 2 precursor (Murine herpesvirus entry protein B) (mhvEB) (Nectin 2) (Poliovirus receptor homolog).			
DE	PVRL2 OR PVS OR PVR OR MPH.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.			
NCBI_Taxid=10090;				
R1	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
EX	MEDLINE=92219365; PubMed=1560525;			
RC	Morrison M.E., Racanelli V.R.;			
RX	"Molecular cloning and expression of a murine homologue of the human poliovirus receptor gene.";			
RT	J. Virol. 66:2807-2813(1992).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RC	STRAIN=C57BL/6; TISSUE=Brain;			
RX	MEDLINE=94179228; PubMed=8132569;			
RT	Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;			
RT	"Amino acid residues on human poliovirus receptor involved in interaction with poliovirus.";			
RL	J. Biol. Chem. 269:8431-8438(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RC	STRAIN=EVB/N; TISSUE=Colon;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshynski S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabey J., Helton E., Kettenman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=92141397; PubMed=10196354;			
RA	Shukla D., Rowe C.L., Dong Y., Racanelli V.R., Spear P.G.;			
RT	"The murine homolog (Mph) of human herpesvirus entry protein B (HvEB) mediates entry of pseudorabies virus but not herpes simplex virus types 1 and 2.";			
RL				

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 9.38761 Seconds
(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187B-2
Perfect score: 2283
Sequence: 1 MASVLPSSGSCCAAAAAA.....AIIAEGGQNNSEKKEYFI 442

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	266.5	11.7	515	1 PVRI_PIG	Q9176 sus scrofa
2	256.5	11.2	517	1 PVRI_HUMAN	O15223 homo sapien
3	247.5	10.8	530	1 PVR2_MOUSE	P32507 mus musculus
4	244	10.7	417	1 PVR_CERAE	P32506 cercopithec
5	242.5	10.6	538	1 PVR2_HUMAN	Q92692 homo sapien
6	240	10.5	417	1 PVR_HUMAN	P15151 homo sapien
7	239	10.5	515	1 PVRI_MOUSE	Q91k6 mus musculus
8	239	10.5	1088	1 NCAL_XENLA	P16170 xenopus lae
9	231	10.1	344	1 NTRI_MOUSE	Q99p10 mus musculus
10	230	10.1	344	1 NTRI_RAT	Q62178 rattus norv
11	228	10.0	344	1 NTRI_HUMAN	Q9p121 homo sapien
12	223.5	9.8	837	1 NCW2_MOUSE	O35136 mus musculus
13	223	9.8	1092	1 NCW2_XENLA	P16335 xenopus lae
14	222	9.7	837	1 NCW2_HUMAN	O15394 homo sapien
15	222	9.7	1242	1 NPHN_HUMAN	Q9q287 mus musculus
16	219	9.6	337	1 OPMC_CHICK	Q98892 gallus gall
17	218.5	9.6	345	1 OPMC_BOVIN	P11834 bos taurus
18	217.5	9.5	583	1 C166_MOUSE	Q61490 mus musculus
19	217	9.5	588	1 C166_CHICK	P42292 gallus gall
20	216.5	9.5	345	1 OPMC_HUMAN	Q14982 homo sapien
21	213.5	9.4	4391	1 PGBM_HUMAN	P98160 homo sapien
22	210.5	9.2	345	1 OPMC_RAT	P32736 rattus norv
23	209	9.2	338	1 LAMP_CHICK	Q98919 gallus gall
24	209	9.2	353	1 CEPU_CHICK	Q99773 gallus gall
25	208	9.1	1493	1 NEOL_MOUSE	P97798 mus musculus
26	207	9.1	847	1 CD22_HUMAN	P20273 homo sapien
27	206.5	9.0	1331	1 CTA2_HUMAN	Q9uhc6 homo sapien
28	206	9.0	702	1 CEAS_HUMAN	P06731 homo sapien
29	205.5	9.0	338	1 SHS1_HUMAN	Q13449 homo sapien
30	205.5	9.0	509	1 SHS1_RAT	P97710 r protein-t
31	205.5	9.0	646	1 MU18_HUMAN	P43121 homo sapien
32	205.5	9.0	1461	1 NEOL_HUMAN	Q92859 homo sapien
33	204	8.9	3707	1 PGBM_MOUSE	Q05793 mus musculus

34	203.5	8.9	862	1 CD22_MOUSE	P35329 mus musculus
35	202	8.8	1377	1 NEOL_RAT	P97603 rattus norv
36	202	8.8	1443	1 NEOL_CHICK	Q90610 gallus gall
37	199.5	8.7	338	1 LAMP_RAT	Q62813 rattus norv
38	199.5	8.7	1241	1 NPHN_HUMAN	O60500 homo sapien
39	197.5	8.7	1234	1 NPHN_RAT	Q9r044 rattus norv
40	197	8.6	583	1 C166_HUMAN	Q13740 homo sapien
41	196	8.6	1091	1 NCAL_CHICK	P13590 gallus gall
42	194	8.5	506	1 SHS1_BOVIN	O46631 bos taurus
43	193	8.5	761	1 NCW2_HUMAN	P13592 homo sapien
44	193	8.5	764	1 ICCR_DROME	Q08180 drosophila
45	193	8.5	848	1 NCAL_HUMAN	P13591 homo sapien

ALIGNMENTS

RESULT 1
PVRI_PIG
ID PVRI_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).
GN PVRL1 OR PRL1 OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Kruppenacher C., Eisenberg R.J., Cohen G.H.;
RT "Porcine HvEC, a member of the highly conserved HvEC/nectin 1 family, is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001)
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC EMBL; AF308632; AAG30281.1; --
DR HSSP; P06907; 1NEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; 1g_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141
FT IG-LIKE V-TYPE.
FT DOMAIN 145 243
FT IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334
FT DOMAIN 437 443

Db 372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR-----GPVVVVTWEGNPVNIITCEVFAH 425

Qy 273 PQPVMTWVRVDDMPQH-----AVLSGP---NIFINNLTNDGTGRCEASNIIVGKAHS 324

Db 426 PR-AAVTFWRDGLPSSNFSGNIKYSPTSSLEVNDSNDFGNCTAINIGHEFS 484

Qy 325 DMLVYVDPPTTIPPTTT 364

Db 485 EFILVQADTPSS---PAIRKVEPYSSTVMIVDFDPDSTGG 521

RESULT 14

T42633

connectin/titin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42633

R:Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma Biochem. Biophys. Res. Commun. 223, 160-164, 1996

A:Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re

A:Reference number: 222221; MUID:96254045; PMID:8660363

A:Accession: T42633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4162 <YAJ>

A:Cross-references: EMBL:D83390; NID:gl513029; PIDN:BAAL1908.1; PID:gl513030

A:Experimental source: breast muscle

C:Keywords: skeletal muscle

Query Match 10.1%; Score 230.5; DB 2; Length 4162;

Best Local Similarity 23.9%; Pred. No. 1.3e-07;

Matches 86; Conservative 60; Mismatches 155; Indels 59; Gaps 15;

Qy 12 CAAAAAAPPGLRLRLLLLSAALIPDGGQNLFTKDVTVIEGEVATISQVKNKSD 71

Db 3453 CIGSVTLRAPPTFVKL-----SDTVVVGTEIQLQAAVEGAQP 3491

Qy 72 SVIQLLNPNROTIFRDFRLKDSRFQLLNFSSELKVSILTNVISIDEGRYFCOLYTD 131

Db 3492 ISVLWLKDKGEII-----RESENLWISYSENVASLKGNAEPTNAGKYICQIKNDAG 3543

Qy 132 -QBSYTTITVLVPPRNLMDIQDQAVE---GEEIEVNCETAMASKPATIRWFKGNTLTK 187

Db 3544 FOEFCFALTVLEP---AVIVKPGPVKVTAGDSCTLECT-VDGTPELTARWFKGNTLS 3598

Qy 188 GKSEVEEWSMDYTVTSQMLKVKHEDDG---VPVICOVHPAVTGNLQ-TQRYLEYQYKRP 243

Db 3599 TDHXY-KISFFNNKVSGLKILNAGLSDSEYTFEVKNSGVKSCTASLQVSDRIMPSPFTR 3657

Qy 244 QVHIQWTPYLOGLTREGDALELTCEAIGKQPQVMTVVRVDDMPQ---HVLVSGP--N 297

Db 3658 K-LKETY-----GQLGSSAVLECKYVGP-PILVSWFHGDGEITSGDKYQATLTDNCS 3709

Qy 298 LFNNLTNDGTGRCEASNIIVGKAHSYMLVYDPTPTI---PPPTTTTTTTTTTTTTTIL 355

Db 3710 LKVNGLQESDMGTYSCTATNAGSDSCAFSLVREPPSFVKXPEFPNVLSGENITFTSIV 3769

RESULT 15

I56551

neurotrinin - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000

C:Accession: I56551

R:Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L. J. Neurosci. 15, 2141-2156, 1995

A:Title: Cloning of neurotrinin defines a new subfamily of differentially expressed neur

A:Reference number: I56551; MUID:95198094; PMID:7891157

A:Accession: I56551

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-344 <RES>

A:Cross-references: EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termil

Query Match 10.1%; Score 230; DB 2; Length 344;

Best Local Similarity 26.2%; Pred. No. 5.6e-09;

Matches 84; Conservative 53; Mismatches 137; Indels 46; Gaps 14;

Qy 29 LLLLFSAALIPDGGQNLFTK---DVTVIEGEVATISQVKNKSDSDSVIQLLNPNROT- 84

Db 29 LRLFLVPTGVPVRSGDATFPKAMDNVTVROGESATLRCTI---DNRVTRVAVLNRSTIL 75

Qy 85 YFRDFRLKDSRFQLLNFSSELKVSILTNVISIDEGRYFCOLYTD-PPOSYTTITVLVP 143

Db 76 YAGNDKWLCDPRVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVS 135

Qy 144 PRNLMDIQDQAVE-EGEEIEVNCETAMASKPATIRWFKGNTLKGKSEVEEWSMDYTVT 202

Db 136 PK-IVEISSDISINEGNNISLACIA-TGRPEPTVTRHISPKAVGVSEDEYLEIQGIT 192

Qy 203 SOLMLKVH---KEDDGVPIVCQVEHPAVTGNLQRYLEYQYKPVQVHIQWTPYLOGL-TR 258

Db 193 REQSGEYECASNDVAAPVVRVN-----VTNVPPYIS-----EAKGTGVP 234

Qy 259 EGDALLETCEAIGKQPQVMTVVRVDDMPQ-----HVLVSGENLFINLNKTNDG 309

Db 235 VGQKGTLOCEASAVPS-AEFQWFKDDKLVGKKGKGVKNRPFSLRITFF--NVSEHDYG 291

Qy 310 TYRCEASNIIVGKAHSYMLY 329

Db 292 NYTCVASNKLIGHTNASIMLF 311

Search completed: May 27, 2004, 09:32:23

Job time : 14.7776 secs


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Db      108 AKQSTGQDTEAELOATLALHGLTVEDEGNCTCEATFPKGVGRGWTWLRVIAKPN-QA 166
QY      150 DIQKDTAVEGEBIEVNCATAMASKPATTIRWFKG-NTELKKGKSEVEBSDMYTVTSQMLK 208
Db      167 EAQKVTFSQDPTTVALCTSKGKPPARISWLSLSDWEAKETQVSGTLAGTIVTSRFTLV 226
QY      209 VHKEDDGVVICQVEHPATGNLQRYLEYQVKQVHIQMTYPLQGLTRGDALELTCE 268
Db      227 PSGRADGVTVTCVKBHESFEFALLPVTLSVRYPPEVSIS-GYDDNMYLGRDTA-TLSCD 284
QY      269 AIGKQPQVMTVVRVDDDEMPQHAVLSGPNLFINNLTNGTYRCEASNIVKHAHSYML 328
Db      285 VRSNEPTGYDWSITSGFTPTSAVAGGSQVLSVHVDLSFNTFTVTVNAVNGRAEQVI 344
QY      329 YVDPPTPIPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 388
Db      345 FVREPTNT-----AGAGATGGI-----IGGIIAIIATA 373
QY      389 LCLLLIILGRYFARHKGTYFTHEAKGADDAADAD-----TALINAE-----G 429
Db      374 VAATGILICRQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 428
QY      430 GQNNSEKKEYF 441
Db      429 ASEHSPKTPYF 440

RESULT 10
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: B44194
A:Reference number: A44194; MUID:93059651; PMID:1331508
A:Accession: B44194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <KOI>
A:Cross-references: GB:S48817
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IM>

Query Match      10.6%; Score 241.5; DB 2; Length 392;
Best Local Similarity 24.0%; Pred. No. 1e-09;
Matches 101; Conservative 60; Mismatches 176; Indels 81; Gaps 16;

QY      13 AAAAAAAPPGLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 68
Db      2 ARTWAARWPP-----LLLTLELSWPPPGTGDIIQAQTPQVPGFLGDSVTLPCYLVQ 55
QY      69 SDDSVIQLINPNR-----QTIYFRDRLPKDSRFOLLNFSSELKVSILTNSV-----I 116
Db      56 MEETHVSQLTWSRHGESSMAVFHTQCPNYSPEKRLFEVFAARLGTDLRDLRMFGLRV 115
QY      117 SDEGRYFCQLYTDPQESYTT---ITVLVPPRNLMIDIKQDTAVEGEBIEV-NCTAMASK 172
Db      116 EDEGNVTC-LFVTFPQGSRSVDIWLRLAKQN-TAEVQK-VOLTGPVPPVAVRCVSTGGR 172
QY      173 PATTIRWFKGNTELKKGSEVEE-----NSDMYTVTSQMLKVKHEDDGVVLCQVEHPAVT 228
Db      173 PPAHITW---HSDLGMPNTSQAGFISGTVTLSLWILVPSQVQDGKSVTCVKEHESFE 229
QY      229 GNLTQRYLEYQVKQVHIQMTYPLQGLTRGDALELTCEAIGKQPQVMTVVRVDDDEMP 288
Db      230 KPQLLTVNLTYYYPEVSIS-GYDDNMYLSQNEA-TITCDARSNPETGYNWSVTMGPLP 287
QY      289 QHAVLSGPNLFINNLTNGTYRCEASNIVKHAHSYMLVYVDPPTTIPPTPTPTPTPTPTPTPT 348
Db      288 PFAVAQAQLLIRPVDKPINTTIFCNVTNALGARQAELTVQVKEGPPSEFGSMSSN----- 343

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QY      349 TTTTILTIITDSRAGEGSRITRAVDHAVIGGVAVVVFAMLCGLLIL-----GRYFAHK 403
Db      344 -----IIIFILGIVILLTLLGIGVYFYRSR 369

RESULT 11
RWHPUD
poliovirus receptor splice form delta precursor - human
N:Alternate names: poliovirus receptor H20B
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A43024; B31496
R:Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Takeuchi, K.; Take-
EMBO J. 9, 3217-3224, 1990
A:Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A:Reference number: S12048; MUID:91006015; PMID:2170108
A:Accession: A43024
A:Molecule type: DNA
A:Residues: 1-392 <KOI>
A:Cross-references: EMBL:X64116
A:Note: 67-A'a was also found
R:Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A:Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and c
A:Reference number: A30910; MUID:89168426; PMID:2538245
A:Accession: B31496
A:Molecule type: mRNA
A:Residues: 1-66, 'A' 68-392 <MEN>
A:Cross-references: GB:M24406
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C:Genetics:
A:Gene: GDB:PVR; PVS
A:Cross-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-392/Product: poliovirus receptor delta #status predicted <MAT>
F:21-343/Domain: extracellular #status predicted <EXT>
F:42-125/Domain: immunoglobulin homology <IM1>
F:159-223/Domain: immunoglobulin homology <IMM2>
F:259-314/Domain: immunoglobulin homology <IMM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-392/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match      10.5%; Score 240; DB 1; Length 392;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 107; Conservative 54; Mismatches 176; Indels 76; Gaps 17;

QY      14 AAAAAAAPPGLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 64
Db      2 ARMAAAWPP-----PPGTG-----DVVVQAQTPQVPGFLGDSVTLPCY 50
QY      65 -QVNKSDSVIQLINPNR-----QTIYFRDRLPKDSRFOLLNFSSELKVSILTNSV----- 115
Db      51 LQVPMETHVSQLTWTRHGESGSMVFTQCPNYSSEKRLFEVFAARLGAELRNASLRM 110
QY      116 -----ISDEGRYFCQLYTDPQESYTT---ITVLVPPRNLMIDIKQDTAVEGEBIEV-NCT 167
Db      111 FGLRVEDEGNYTC-LFVTFPQGSRSVDIWLRLAKQN-TAEVQK-VOLTGPVPPVAVRCV 167
QY      168 AMASKPATTIRWFKGNTELKKGSEVEE-SDMYTVTSQMLKVKHEDDGVVLCQVEHPA 226
Db      168 STGGRPPAQLTHSD-LGMPNTSQAGFISGTVTLSLWILVPSQVQDGKSVTCVKEHES 227
QY      227 VTGNLTQRYLEYQVKQVHIQMTYPLQGLTRGDALELTCEAIGKQPQVMTVVRVDDDE 286
Db      228 FEKPOLLTVNLTYYYPEVSIS-GYDDNMYLSQNEA-TITCDARSNPETGYNWSVTMG 285
QY      287 MPQHAVLSGPNLFINNLTNGTYRCEASNIVKHAHSYMLVYVDPPTTIPPTPTPTPTTT 346

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	Query Match	10.6%	Score 242.5;	DB 2;	Length 538;
	Best Local Similarity	22.6%;	Pred. No. 1.3e-09;		
	Matches 111;	Conservative 66;	Mismatches 202;	Indels 113;	Gaps 17;
QY	10	SQAAAAAAPPGLRLRLLLLLSAAALPTGDGONLFTKDVTVEIEVATISQVNKS	69		
Db	2	ARAAALLPSRPPTLLWPPLLLL-----LLENG-AQDVAVQVLPEVRG-----QLGGT	49		
QY	70	DDSVIQLLNPP-----NRQTYFRDFPFLKDSRF-----QLINFS	104		
Db	50	VELPCHLLLPVPGLYISLVTWQRDPAPANQNIV--AAPHKMGSPFPSPKPGSERLSFVS	107		
QY	105	S-----ELKVSLTNVISIDEGRYCQLYTDIP--PQESYTITVLVPRNLMI	149		

F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.9%; Score 248; DB 2; Length 518;
Best Local Similarity 25.4%; Pred. No. 4.9e-10;
Matches 105; Conservative 60; Mismatches 154; Indels 94; Gaps 20;

QY 74 IQLNPNRQTYFRDRLKDSRQFLLNFSSELKSVLTNVSISDEGRYFQQLYDPP-- 131
DB 78 VAIINPSMGVSLAPYR-----ERVEFLRPSFTDGTIRLSRLELEDEGVYICFATFTGN 133

QY 132 QESYTIIVLPPRLMIDIKD-TAVEGEELV---NCTAMASKPATIRWFKNTELK 187
DB 134 RESQNLTVMAKPTNWIETGQAVLRKQDDKVLVATCTSANGKPPSVGSM---ETRLK 190

QY 188 GKSEV--EWSDM--YVTSQMLKVKHEDDGVVICOVEHPAVTGNLQTOY-----LE 238
DB 191 GEARVPGSGTPMAPVTVISRYLVPSEARHQSLACIV-----NYHMDRFKESULTIN 243

QY 239 VOYKPOVHIQ---MTYPLQGLTREGDALELTCEALGKQPQVMVTVVRVDDDEMPQHAVLSG 295
DB 244 VOYEPEVTIEGFGNWLQRM-----VKLTCKADANPPATEYHWTTLNGLSLPKGVEAQN 298

QY 296 ENLFINN-LNKTNGTYRCEASNIYGVKAHSDYMLVYVDPTTIPPTTTTTTTTTTI 354
DB 299 RTLFKFGPINSLAGTYICEATNPIGTRSGQGVNITEFPTTPPPE----- 345

QY 355 LTIITDSRAGEGSIKRAVDHAVIGVAVVVFAMLCILILIGRYFA---RH--KGYFT 408
DB 346 ---HGRAG-----PVPTALIGGVAGSI---LLVLIVGVIVVALRRRHTFKGDYST 392

QY 409 -----HKAQA-----DDAADATAIINAGGQNNSEKKE 439
DB 393 KKHVYNGYSGKAGIPOHPPMAQNLOYPDDSDDEKKA--GPLGGSSYEEREE 443

RESULT 5
A53437
poliovirus receptor mPVR - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
R:Ack: J. Koike, S. Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with p
A:Reference number: A53437; MUID:94179228; PMID:8132569
A:Accession: A53437
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <ACK>
A:Cross-references: GB:D26107; NID:9475017; PIDN:BAA05103.1; PID:9825507
A:Experimental source: C57/BL6, brain
A:Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIPI:146667)
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 247.5; DB 2; Length 530;
Best Local Similarity 22.1%; Pred. No. 5.5e-10;
Matches 91; Conservative 63; Mismatches 166; Indels 91; Gaps 14;

QY 15 AAAAAAPP-----LRLRLMLLSAALIPGTGQNLFTKDVTVIRGEV---ATISQV 66
DB 2 ARAAVLPPSLRSLPTLPLPLLL-----LLETGAQDVRVRLPEVRGRLGTVLPCHL 56

QY 67 -----NKSDSVIQLNPNRQTYFRDRLKDSRFOL-----LNFSS 105
DB 57 LPPTTERVSQVTQRLDGTVAAFHPS-----FGVDFNFSQFSKRLSFVRARPETNADLR 112

QY 106 ELKVLNVSISDRGRFCQLYTPD--POESYTTITVLVPPRLMIDIKD-TAVEGEIE 163
DB 113 DATLAFRLGRVEDEGNTCEPATFNGTRGVTLWRIAQPN-----HAAQEV 163

QY 164 V-----NCTAMASKPATIRFKG-NTELKSKSEVEESDMYTVTSQMLKVKHEDD 214

DB 164 IGQSVAVARCVSTGGRPPARITWISSLGSEAKDTQEBGIQAGTVTIISRYSLVVPVGRAD 223

QY 215 GVPVICOVEHPAVTGNLQTOYRLEVQVKPQVHIOMTYPLQGLTREGDALELTCEALGKQP 274

DB 224 GVKVTCRVEHSEFBEPILLPVTLRVYRPEVISIS-GYDDNWNYLGRSEAI-LTCDVRSNPE 281

QY 275 PVMVTVVRVDDDEMPQHAVLSQPNLFINNLTNGTYRCEASNIYGVKAHSDYMLVYVDPP 334

DB 232 PTDDWSTTSVFPASAVAQSQQLVHSVRWNTTFTCTATNAVGTGRAQVILVRESP 341

QY 335 TTIPPTTTTTTTTTTTTTTTTTITITDSRAGEGSIKRAVDHAVIGVAVV 385

DB 342 ST-----AGAGATCGI-----IGGIIAAII 361

RESULT 6
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: A44194
R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A:Title: A second gene for the African green monkey poliovirus receptor that has no put.
A:Reference number: A44194; MUID:93059651; PMID:1331508
A:Accession: A44194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-417 <KOI>
A:Cross-references: GB:S48777
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: transmembrane protein
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 10.7%; Score 244; DB 2; Length 417;
Best Local Similarity 23.5%; Pred. No. 7.2e-10;
Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;

QY 13 AAAAAAPPCLRLRLMLLSAALIPGTGQNLFTKDVTV--IEGEVATISC--QUNK 68

DB 2 ARTWAAWPP-----LLLTLLELWSPPPTGDIIVQAPTQVPGFLGDSVTLPCYLQVPG 55

QY 69 SDDSVIQLNPNR-----QTYFRDRLKDSRQFLLNFSSELKSVLTNVS-----I 116

DB 56 MEETHVSQLTWSRHGESSMAVPHQTQGPVSEPKRLEFVAARLGTSLRDLASLRFGLRV 115

QY 117 SDEGRYFCQLYTDPDQSYTT---ITVLVPPRLMIDIKD-TAVEGEIEV-NCTAMASK 172

DB 116 EDEGNYTC-LFVTFPQGRSVDIWLRLAKPON-TAEVQK-VQLTGKPPVVARCVSTGR 172

QY 173 PATTIRWFKNTELKSKSEVEE---WSDMYTVTSQMLKVKHEDDGVVICOVEHPAVT 228

DB 173 PPAHITW---HSDLGGMNTSQAPFLSGVTVTSLMILVPSQVDGKSVTCRVEHSEFE 229

QY 229 GNLTQRYLEVQVKPQVHIOMTYPLQGLTREGDALELTCEALGKQPQVMVTVVRVDDDEMP 288

DB 230 KPQLLTNLVTVYRPEVISIS-GYDDNWNYLQNEA-TLTCDAASNPEPTGYNWSITWGFLP 287

QY 289 QHAVLSQPNLFINNLTNGTYRCEASNIYGVKAHSDYMLVYVDPTTIPPTTTTTTTTT 348

DB 288 PFVAQAQALLIRPVDKPIINTTFTICNVNALGARQABLTQVKEGPPSEPSGSSN--- 343

QY 349 TTTTITITITDSRAGEGSIKRAVDHAVIGVAVVVFAMLCILIL-----GRYFARHK 403

DB 344 -----IIIFLIGVILLLTLIGIGVYFYSR 369

QY 404 GT-----YFTEAKGADDAADATAIINAGGQNNSEKKE 439

DB 370 CSREFLWCHLSSEBHASA-----SANGYISVSDVSRE 404

RESULT 7
HLMSP3

R. Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20992
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-5175 <WIL>
 A:Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
 A:Experimental source: clone F15G9
 R:Kershaw, J.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z22396
 A:Accession: T43290
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-5198 <VOG>
 A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20993

Query Match 11.5%; Score 263.5; DB 2; Length 5175;
 Best Local Similarity 24.6%; Pred. No. 7.6e-10;
 Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;

QY 52 VTVEGEVATISQVKNKSDSDSVIQLNPNRTIYFRDPRP-----KDSRFOLLNFSSEL 107
 Db 2200 VTAIKGALPFPKCPID--DDK-----NFKGQIIWLRYNPIDLEAEDARITRL---SNDR 2249
 QY 108 KSVLTNSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIQD-TAVEGEEIEVN 165
 Db 2250 RLTLNVENDEGOYSCRVKNDAgensFDFKAVLVPTTIIMLDKKNKTAVEHSTVTL 2309
 QY 166 CTAMASKPATIRWFKG-----NTLKGKSEVEEWSDMYTVTSQMLKVKH 211
 Db 2310 CPA-TGKPEPDITWFKDGEALHNIADIIPNGELNG-----NQLKITRIK 2354
 QY 212 EDDGVPIQVEHPVATGNLTQRYLEVQYKPVH---IQMTYPLQGLTREGDALELTCE 268
 Db 2355 EGDAGKYTCBADNSA--GSVEQDVNVNVTIPKIEKDGPISDYESQ---QNERVVISCP 2408
 QY 269 AIGKPPQVMVTVRVDDMPQHAVL-----SGPNLFNNLNKTDNGTYRCEASNIVGKAHS 324
 Db 2409 VYARP-PAKITLWAKGPKLQSDKFVKTSAHQKLYLFKLRDTSKTYCTATNEAGTDKR 2467
 QY 325 DYMLYVYDPTTIPP-----PTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGE 365
 Db 2468 DFKVSMVLVAPSFDEFNIVRRITVNSGNPSTLHCPAKGSPSTITWLKDGNAIE 2520

RESULT 3
 T43290
 hemicentin precursor - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43290; T20993; T24734
 R:Voegel, B.E.; Hedgecock, E.M.
 submitted to the EMBL Data Library, June 1998
 A:Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
 A:Reference number: Z22396
 A:Accession: T43290
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-5198 <VOG>
 A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
 R:Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20993

A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <WIL>
 A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
 A:Experimental source: clone F15G9
 R:Kershaw, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19929
 A:Accession: T24734
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <W12>
 A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
 A:Experimental source: clone T09B9
 C:Genetics:
 A:Gene: hlm-4; F15G9.4b
 A:Map position: X
 A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
 : 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
 Query Match 11.5%; Score 263.5; DB 2; Length 5198;
 Best Local Similarity 24.6%; Pred. No. 7.6e-10;
 Matches 87; Conservative 66; Mismatches 129; Indels 71; Gaps 15;

QY 52 VTVEGEVATISQVKNKSDSDSVIQLNPNRTIYFRDPRP-----KDSRFOLLNFSSEL 107
 Db 2200 VTAIKGALPFPKCPID--DDK-----NFKGQIIWLRYNPIDLEAEDARITRL---SNDR 2249
 QY 108 KSVLTNSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIQD-TAVEGEEIEVN 165
 Db 2250 RLTLNVENDEGOYSCRVKNDAgensFDFKAVLVPTTIIMLDKKNKTAVEHSTVTL 2309
 QY 166 CTAMASKPATIRWFKG-----NTLKGKSEVEEWSDMYTVTSQMLKVKH 211
 Db 2310 CPA-TGKPEPDITWFKDGEALHNIADIIPNGELNG-----NQLKITRIK 2354
 QY 212 EDDGVPIQVEHPVATGNLTQRYLEVQYKPVH---IQMTYPLQGLTREGDALELTCE 268
 Db 2355 EGDAGKYTCBADNSA--GSVEQDVNVNVTIPKIEKDGPISDYESQ---QNERVVISCP 2408
 QY 269 AIGKPPQVMVTVRVDDMPQHAVL-----SGPNLFNNLNKTDNGTYRCEASNIVGKAHS 324
 Db 2409 VYARP-PAKITLWAKGPKLQSDKFVKTSAHQKLYLFKLRDTSKTYCTATNEAGTDKR 2467
 QY 325 DYMLYVYDPTTIPP-----PTTTTTTTTTTTTTTTTTTTTTTTTTSDRAGE 365
 Db 2468 DFKVSMVLVAPSFDEFNIVRRITVNSGNPSTLHCPAKGSPSTITWLKDGNAIE 2520

RESULT 4
 JC4024
 poliovirus receptor-related protein precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
 C:Accession: JC4024
 R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubo
 Gene 155, 261-285, 1995
 A:Title: Complementary DNA characterization and chromosomal localization of a human gene
 A:Reference number: JC4024; MUID:95237621; PMID:7721102
 A:Accession: JC4024
 A:Molecule type: mRNA
 A:Residues: 1-518 <LOP>
 A:Cross-references: EMBL:X76400; NID:g732795; PIDN:CAAS3980.1; PID:g732796
 C:Genetics:
 A:Gene: GDB:PVRR1
 A:Cross-references: GDB:583951
 A:Map position: 11q23-11q24
 C:Superfamily: poliovirus receptor; immunoglobulin homology
 C:Keywords: glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
 F:356-379/Domain: transmembrane #status predicted <TMW>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 12.7776 Seconds
(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-2
Perfect score: 2283
Sequence: 1 MASVLPSSGSCAAAAAAA.....AIINAEQQNSSEKKEYFI 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	11.7	407	T08732	hypothetical prote
2	263.5	11.5	5175	T20992	hypothetical prote
3	263.5	11.5	5198	T43290	hemocentin prote
4	248	10.9	518	JC4024	poliovirus recepto
5	247.5	10.8	530	A53437	poliovirus recepto
6	244	10.7	417	A44194	poliovirus recepto
7	244	10.7	467	HLMSFP3	poliovirus recepto
8	243	10.6	725	JE00099	PRR2 delta - human
9	242.5	10.6	538	I68093	poliovirus recepto
10	241.5	10.6	392	B44194	poliovirus recepto
11	240	10.5	392	RWHUPA	neural cell adhesi
12	240	10.5	417	1	poliovirus recepto
13	239	10.5	1088	1	poliovirus recepto
14	230.5	10.1	4162	T42633	neural cell adhesi
15	230	10.1	344	I56551	connectin/titin -
16	226	9.9	812	B42632	neurotrimin - rat
17	226	9.9	932	A42632	cell adhesion mole
18	225	9.9	7962	I38346	cell adhesion mole
19	223.5	9.8	1011	TJ3669	elastic titin - hu
20	223	9.8	725	JE0100	neuromusculin - fr
21	223	9.8	1092	1	neural cell adhesi
22	222	9.7	478	I53960	PRR2 alpha - human
23	218.5	9.6	345	S03199	opitoid-binding pro
24	218.5	9.6	588	A45254	surface glycoprote
25	217	9.5	588	JH0506	adhesion molecule
26	216.5	9.5	345	JC4025	opitoid-binding cel
27	216	9.5	765	A42632	cell adhesion mole
28	214	9.4	4391	A38096	perlecan precursor
29	210.5	9.2	345	JC1239	opitoid-binding pro

30	209.5	9.2	584	2	I50419	s-gicerin precurs
31	209	9.2	338	2	JC5519	50K glycoprotein p
32	206	9.0	702	2	A36319	carcinoembryonic a
33	205.5	9.0	338	2	JC4776	limbic-system-asso
34	205.5	9.0	646	2	I38049	cell surface glyco
35	204.5	9.0	338	2	JC1238	opitoid-binding pro
36	204	8.9	3707	2	I18252	heparan sulfate pr
37	203	8.9	1323	2	PN0568	connectin 3B - chi
38	202.5	8.9	862	2	I49583	differentiation an
39	202.5	8.9	868	2	A46512	CD22 homolog/B lym
40	202	8.8	847	2	JH0371	B-cell adhesion pr
41	202	8.8	1443	2	I50600	neogenin - chicken
42	199.5	8.7	1241	2	T37190	nephrin - human
43	197	8.6	583	2	I39428	alcam - human
44	196	8.6	1091	1	IUCHNL	neural cell adhesi
45	195.5	8.6	1612	2	T30805	dutt1 protein - mo

ALIGNMENTS

RESULT 1

T08732
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C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08732
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OTT>
A:CROSS-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFP566B0846
C:Genetics:
A:Note: DKFP566B0846.1

Query Match 11.7%; Score 268; DB 2; Length 407;
Best Local Similarity 26.7%; Pred. No. 1.4e-11;
Matches 84; Conservative 60; Mismatches 123; Indels 48; Gaps 13;

QY	120	GRYFCOLYTD--POESYTTITVLVPPRLMIDIOKTAVEG--EEIVNCTAMASKPAT	175
DB	2	GXVICKAVTFPLGNAGSSTTVVLVEPTVSLIK-GPDSLIDGNETVAICIAATGKPA	60
QY	176	TTRWPKGNTLKGKSEVEWSDMY-----TVTSQMLKVHKEDDGVPIVCQVEHPAVTGN	230
DB	61	HIDW-EGDL-----GEMESTTTSFPNETATILISQYKLPFTRFARGRRITCVVKGHPALEKD	114
QY	231	LQTRVLEVOYKQVHIQMTYPLQGLTRGDALELTCEAIGKPPQVMTWVRVDDMPQH	290
DB	115	IYSLFDLQYAPEVSVTVGDGNWFWVGRKG--VNLKCNADANPPFPFKSVWSRLDGQWPDG	172
QY	291	AVLSGPNL-FINNLKNTDNGTYRCEASNIVGKAHSDMYLVVYDDP--TTTP-----PTT	342
DB	173	LLASDNLHFVHPLFNYSGVVICKVTSLGORSQOKVYIISDPPTTTTLQTIQWHPST	232
QY	343	TTTTTTTT-----TTTILTIITDSRAGSGSIRAVDHAIVGGVAVVWVAMCLLI-	393
DB	233	ADIEDLATEPKLPPPLSLATI-----KDDTIATIASVVGALFVLVSLVGLGIFC	285
QY	394	-----ILGRYFAH 402	
DB	286	YRRRTFRGDYFAKN 300	

RESULT 2

T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20992; T24733

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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-84

Query Match      90.9%; Score 2059; DB 10; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLILLLLFACCCWAPGAGNLSQDGYWQEQDLELGLTAPLDEAISSTWSSPDML 60
Db 1 MGAPAAASLLILLLLFACCCWAPGAGNLSQD----- 29

QY 61 ASQDSQPWTSDETVVAGTIVVLKQVQKHEDSSLOWNSPAQQTLFYGEKRALRDNEIQIV 120
Db 30 ---DSQFWSDETVVAGTIVVLKQVQKHEDSSLOWNSPAQQTLFYGEKRALRDNEIQIV 86

QY 121 TSTPHELSSISNVALADGEYTCSTFTWVRTAKSLVTVLGIPOKPIITGYKSSLRKX 180
Db 87 TSTPHELSSISNVALADGEYTCSTFTWVRTAKSLVTVLGIPOKPIITGYKSSLRKX 146

QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKPTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKPTVSSSVTFQVTRDDGAS 206

QY 241 IVCNVNHESLKGADRSSTORIEVLVYPTTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 300
Db 207 IVCNVNHESLKGADRSSTORIEVLVYPTTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 266

QY 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGYGTATSNMGSKAYYTLNVNDPSPVPSSS 360
Db 267 WEKEGSVPPLKMTQESALIFPFLNKSDSGYGTATSNMGSKAYYTLNVNDPSPVPSSS 326

QY 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLI RHKGYLT HEAKGSDDAPDADTAI NAEGG 420
Db 327 STYHAIIGGIVAFIVFLLLMILIFLGHYLI RHKGYLT HEAKGSDDAPDADTAI NAEGG 386

QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398
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Search completed: May 27, 2004, 09:52:23
Job time : 38.7009 secs

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.8%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCCWAPGAGNLSQDGYWQEDLELGTLLAPLDEAISSTWSSPDM 60
DB 1 MGAPAAASLLLLLLFACCCWAPGAGNLSQD----- 29
QY 61 ASQDSQPTSDTETVAGGTIVLKCQVKDHDSSLOWNSPAQOTLYFGKRALRDNRIQLV 120
DB 30 ---DSQPTSDTETVAGGTIVLKCQVKDHDSSLOWNSPAQOTLYFGKRALRDNRIQLV 86
QY 121 TSTPHELSSISNVALADGEVTCSTFTWVTRAKSLVTLVGIPOKPIITGYKSSLRKD 180
DB 87 TSTPHELSSISNVALADGEVTCSTFTWVTRAKSLVTLVGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKADRSSTORIEVLVPTAMIRDPDPHPPREGOKLLHCEGRNPVPQQYL 300
DB 207 IVCSVNHESLKADRSSTORIEVLVPTAMIRDPDPHPPREGOKLLHCEGRNPVPQQYL 266
QY 301 WEKGSVPLKWTQTSALIFPFLNKSDSTGYCTATSNMGSKAYVTLNNDPSPVPS 360
DB 267 WEKGSVPLKWTQTSALIFPFLNKSDSTGYCTATSNMGSKAYVTLNNDPSPVPS 326
QY 361 SYTHAIGGIVAFIVFLLLIMLIFLGHYLRHKGYLTHEAKGSDDAPDADTAIINAE 420
DB 327 SYTHAIGGIVAFIVFLLLIMLIFLGHYLRHKGYLTHEAKGSDDAPDADTAIINAE 386
QY 421 QSGGDDKEYFI 432
DB 387 QSGGDDKEYFI 398

US-09-907-841-84

RESULT 15

US-09-904-011-84

Sequence 84, Application US/09904011

Publication No. US20030003530A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

ACIDS Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,011

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

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QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 13
US-09-824-84
; Sequence 84, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-84

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Loca. Similarity 92.1%; Pred. No. 5, 5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSDQGYOQDLELGLTAPLDEAISTVWSSPDML 60
Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSDQGYOQDLELGLTAPLDEAISTVWSSPDML 60
QY 61 ASQDSQPWTSDETVAGGTVVLKCOVKDHEDSSLOWNSPAAQOTLYGKKAALDRNRIQLV 120
Db 30 ---DSQPWTSDETVAGGTVVLKCOVKDHEDSSLOWNSPAAQOTLYGKKAALDRNRIQLV 86
QY 121 TSTPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
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Db 207 IVCSVNHESLKGADRTSQRIEVLVYPTAMIRDPDPHREGOKLLHCEGRGNVPQQYL 266
QY 301 WEKGVVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYVTLNVNDFSPVSSS 360
Db 267 WEKGVVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYVTLNVNDFSPVSSS 326
QY 361 SYTHAIIIGGIVAFIVFLLIMLIFLGHYLIIRKGYTLTHEAGSDPADADTAIINAE 420
Db 327 SYTHAIIIGGIVAFIVFLLIMLIFLGHYLIIRKGYTLTHEAGSDPADADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 14
US-09-907-841-84
; Sequence 84, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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US-09-778-187B-10

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLLLFACCCWAPGANLSODGYWQEQDLELGTIAPLDEAISSTVWSSPDM 60
DB 1 MGAPAAASLLLLLLLLFACCCWAPGANLSOD----- 29
QY 61 ASQSQPWTSDTETVAGTGVVLKCOVKDHDSSLOWSPAQOTLYFGEKRALDNRIO 120
DB 30 ---DSQPWTSDTETVAGTGVVLKCOVKDHDSSLOWSPAQOTLYFGEKRALDNRIO 86
QY 121 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLGIPQKPIITGYKSLREK 180
DB 87 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLGIPQKPIITGYKSLREK 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 300
DB 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 266
QY 301 WEKESGVPPLKMTQESALIFPFLNKS DSGTGTATSNMGSKYKAYITLVNNDPSPVPSSS 360
DB 267 WEKESGVPPLKMTQESALIFPFLNKS DSGTGTATSNMGSKYKAYITLVNNDPSPVPSSS 326
QY 361 STYHAIIGGIIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAIINAE 420
DB 327 STYHAIIGGIIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAIINAE 386
QY 421 QSGGDDKKEYPI 432
DB 387 QSGGDDKKEYFI 398

RESULT 12

US-09-902-853-84

; Sequence 84, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE OF INVENTION: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLLLFACCCWAPGANLSODGYWQEQDLELGTIAPLDEAISSTVWSSPDM 60
DB 1 MGAPAAASLLLLLLLLFACCCWAPGANLSOD----- 29
QY 61 ASQSQPWTSDTETVAGTGVVLKCOVKDHDSSLOWSPAQOTLYFGEKRALDNRIO 120
DB 30 ---DSQPWTSDTETVAGTGVVLKCOVKDHDSSLOWSPAQOTLYFGEKRALDNRIO 86
QY 121 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLGIPQKPIITGYKSLREK 180
DB 87 TSTPHELISISINVALADEGYTCISFTMPVTRTAKSLVTLGIPQKPIITGYKSLREK 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 300
DB 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 266
QY 301 WEKESGVPPLKMTQESALIFPFLNKS DSGTGTATSNMGSKYKAYITLVNNDPSPVPSSS 360
DB 267 WEKESGVPPLKMTQESALIFPFLNKS DSGTGTATSNMGSKYKAYITLVNNDPSPVPSSS 326
QY 361 STYHAIIGGIIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAIINAE 420
DB 327 STYHAIIGGIIVAFIVFLLIMLIIFLGHYLIHKGTYLTAEKGSDDADPADTAIINAE 386

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-84

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQEDLELGLTAPLDEAISSTVWSSPDML 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQD----- 29
QY 61 ASQDSQPWTSDETVVAGGTWVLCQVKDHEDSSLOWSNPAQOTLYFGEKRALRDNRQLV 120
DB 30 ---DSQPWTSDETVVAGGTWVLCQVKDHEDSSLOWSNPAQOTLYFGEKRALRDNRQLV 86
QY 121 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
DB 87 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGKLLHCEGRGNPVPQQYL 300
DB 207 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGKLLHCEGRGNPVPQQYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYTYTLNVNDPSPVSSS 360
DB 267 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYTYTLNVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLIMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 420
DB 327 STYHAIIGGIVAFIVFLIMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 386
QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

RESULT 10
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1

; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQEDLELGLTAPLDEAISSTVWSSPDML 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQD----- 29
QY 61 ASQDSQPWTSDETVVAGGTWVLCQVKDHEDSSLOWSNPAQOTLYFGEKRALRDNRQLV 120
DB 30 ---DSQPWTSDETVVAGGTWVLCQVKDHEDSSLOWSNPAQOTLYFGEKRALRDNRQLV 86
QY 121 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
DB 87 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGKLLHCEGRGNPVPQQYL 300
DB 207 IVCSNVHESLKGADRSQRIEVLVYPTAMIRPDPPHREGKLLHCEGRGNPVPQQYL 266
QY 301 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYTYTLNVNDPSPVSSS 360
DB 267 WEKESVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYTYTLNVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLIMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 420
DB 327 STYHAIIGGIVAFIVFLIMLIFLGHYLRHKGYLTHEAKGSDDAPADTAIINAEQG 386
QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

RESULT 11
US-09-778-187B-10
; Sequence 10, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 398
; TYPE: PRT
; ORGANISM: homo sapiens

```
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; TYPE: PRT
; LENGTH: 398
; ORGANISM: Homo sapiens
US-09-909-088B-84

Query Match          90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.8%; Pred. No. 5.Se-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY      1  MGAPASLLLLLLLFFACCGAGCANLSQDGYQDLELGTPLAPDEALSSVTSWSPDML 60
Db      1  MGAPASLLLLLLLFFACCGAGCANLSQD----- 29
QY      61  ASQDSQFWSDETVAAGTIVLKCQVKDHDSSLOWNSPAAQTLTYFGKRALRDNRILQV 120
Db      30  ---DSQPWTSDETVAAGTIVLKCQVKDHDSSLOWNSPAAQTLTYFGKRALRDNRILQV 86
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QY      121  TSTPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db      87  TSTPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY      181  TATINCOSGSKPAARLTWRKQDQLHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db      147  TATINCOSGSKPAARLTWRKQDQLHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206
QY      241  IVCSVNHESLKADRSSTQRIEVLVYPTAMIRDPDPHPPREGOKLLHCEGRGNPVPQOYL 300
Db      207  IVCSVNHESLKADRSSTQRIEVLVYPTAMIRDPDPHPPREGOKLLHCEGRGNPVPQOYL 266
QY      301  WEKEGSVPPLKMTQESALFFPLNKSDSGTYGCTATSNMGSKYKAYYTLNVNDSPPVSSS 350
Db      267  WEKEGSVPPLKMTQESALFFPLNKSDSGTYGCTATSNMGSKYKAYYTLNVNDSPPVSSS 326
QY      361  STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPADATAIINAE 420
Db      327  STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTLYLTHEAKGSDDAPADATAIINAE 386
QY      421  QSGGDDKKEYFI 432
Db      387  QSGGDDKKEYFI 398
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RESULT 9

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US-09-905-291A-84
; Sequence 84, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
```

Db 147 TATLNCSSGSKPAARLTWRKQDQLHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQSRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 300
Db 207 IVCSVNHESLKGADRSQSRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 266
QY 301 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 360
Db 267 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDADPDTAIINAE 420
Db 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDADPDTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 7

US-09-909-320-84
; Sequence 84, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-84
Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSODGYWQEODLELGTAPLDEAISSTVWSSPDML 60
Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSQD----- 29
QY 61 ASQDSQFWSDETAVAGTIVLKCQVKHEDSSLOWNPAQOTLYFGEKRALDNRIOVLV 120
Db 30 --DSQPWTSDETAVAGTIVLKCQVKHEDSSLOWNPAQOTLYFGEKRALDNRIOVLV 86
QY 121 TSTPHLSISISNVALADEGETCSIFTMPVTAKSALTIVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHLSISISNVALADEGETCSIFTMPVTAKSALTIVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKQDQLHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKQDQLHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQSRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 300
Db 207 IVCSVNHESLKGADRSQSRIEVLVYPTAMTRPDPHPHREGQKLLHCEGRGNVPVQQYL 266
QY 301 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 360
Db 267 WEKEGSPVPLKMTQESALIFPFLNKSQSGTGCCTATSNMGSYKAYITLVNDPSPVSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDADPDTAIINAE 420
Db 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDADPDTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 8

US-09-909-088B-84
; Sequence 84, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
QY 241 IVCNVNHSILKGDRTSRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
Db 241 IVCNVNHSILKGDRTSRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
QY 301 WEKESVPLPKMTQESALIFPFLNKS DSGTYGCTATSNMGSYKAYTTLNVNDFSPVSSS 360
Db 301 WEKESVPLPKMTQESALIFPFLNKS DSGTYGCTATSNMGSYKAYTTLNVNDFSPVSSS 360
QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTATLNAEGG 420
Db 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTATLNAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 5
US-10-302-041-2
; Sequence 2, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; PRIOR FILING DATE: 2002-11-21
; PRIOR FILING DATE: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR FILING DATE: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-2

Query Match 100.0%; Score 2264; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLLLLLLLFFACCCWAPGAGANLSQDGYWQEDLEGLTAPLDEAISSTVWSSPDML 60
Db 1 MGAPASLLLLLLLFFACCCWAPGAGANLSQDGYWQEDLEGLTAPLDEAISSTVWSSPDML 60
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Db 61 ASQDSQPWTSDETAVAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDNRILV 120
QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
QY 241 IVCNVNHSILKGDRTSRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
Db 241 IVCNVNHSILKGDRTSRIEVLVYPTAMIRPDPPHPRREGQKLLHCEGRGNVPQQYL 300
QY 301 WEKESVPLPKMTQESALIFPFLNKS DSGTYGCTATSNMGSYKAYTTLNVNDFSPVSSS 360
Db 301 WEKESVPLPKMTQESALIFPFLNKS DSGTYGCTATSNMGSYKAYTTLNVNDFSPVSSS 360
QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTATLNAEGG 420

Db 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAKGSDDDPADTATLNAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 6
US-09-745-763-102
; Sequence 102, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 219
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/745,763
; FILING DATE: 18-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-745-763-102

Query Match 90.9%; Score 2059; DB 9; Length 398;
Best Local Similarity 92.1%; Pred. No. 5.5e-160;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPASLLLLLLLFFACCCWAPGAGANLSQDGYWQEDLEGLTAPLDEAISSTVWSSPDML 60
Db 1 MGAPASLLLLLLLFFACCCWAPGAGANLSQD----- 29
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Db 30 ---DSQPTSDTETVAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDNRILV 86
QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240

;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/049,373
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,875
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/049,374
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,917
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,949
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,974
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,883
;; PRIOR FILING DATE: 1997-06-06
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;; PRIOR FILING DATE: 1997-06-06
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;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,963
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,877
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/048,878
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/068,054
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,064
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,053
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/070,923
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/073,160
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,159
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,165
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/073,164
;; PRIOR FILING DATE: 1998-01-30
;; PRIOR APPLICATION NUMBER: 60/085,925
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,921
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,923
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/085,922
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/092,921
;; PRIOR FILING DATE: 1998-07-15
;; PRIOR APPLICATION NUMBER: 60/094,657
;; PRIOR FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1245
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 361
;; LENGTH: 432
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-933-767-361

Query Match 100.0%; Score 2264; DB 10; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAAPASLLLLLLFACCCWAPGAGANLSDQGYWQEOQDLGLTGLAPLDEAISTVWSSPDML 60
DB 1 MGAAPASLLLLLLFACCCWAPGAGANLSDQGYWQEOQDLGLTGLAPLDEAISTVWSSPDML 60
QY 61 ASQDSQPWTSDETVVAGTGVVLKQVQKHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120

DB 61 ASQDSQPWTSDETVVAGTGVVLKQVQKHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120
QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSLREKD 180
DB 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSLREKD 180
QY 131 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
DB 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKGAADRSTQRIEVLVYTPAMIRPDPHPREGQKLLHCEGNGNVPQOYL 300
DB 241 IVCSVNHESLKGAADRSTQRIEVLVYTPAMIRPDPHPREGQKLLHCEGNGNVPQOYL 300
QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYAYTLNVNDPSPVPSS 360
DB 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKAYAYTLNVNDPSPVPSS 360
QY 361 STVHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHKAGSDDDADADATINAE 420
DB 361 STVHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHKAGSDDDADADATINAE 420
QY 421 QSGGDDKKYFI 432
DB 421 QSGGDDKKYFI 432

RESULT 4
US-10-161-572-49
;; Sequence 49, Application US/10161572
;; Publication No. US20030087266A1
;; GENERAL INFORMATION:
;; APPLICANT: EXELIXIS, INC.
;; TITLE OF INVENTION: IGS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
;; FILE REFERENCE: EX02-097C-PC
;; CURRENT APPLICATION NUMBER: US/10/161,572
;; CURRENT FILING DATE: 2002-06-03
;; PRIOR APPLICATION NUMBER: US 60/296,076
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: US 60/328,605
;; PRIOR FILING DATE: 2001-10-10
;; PRIOR APPLICATION NUMBER: US 60/338,733
;; PRIOR FILING DATE: 2001-10-22
;; PRIOR APPLICATION NUMBER: US 60/357,253
;; PRIOR FILING DATE: 2002-02-15
;; PRIOR APPLICATION NUMBER: US 60/357,600
;; PRIOR FILING DATE: 2002-02-15
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 49
;; LENGTH: 432
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-161-572-49

Query Match 100.0%; Score 2264; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAAPASLLLLLLFACCCWAPGAGANLSDQGYWQEOQDLGLTGLAPLDEAISTVWSSPDML 60
DB 1 MGAAPASLLLLLLFACCCWAPGAGANLSDQGYWQEOQDLGLTGLAPLDEAISTVWSSPDML 60
QY 61 ASQDSQPWTSDETVVAGTGVVLKQVQKHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120
DB 61 ASQDSQPWTSDETVVAGTGVVLKQVQKHEDSSLOWSNPAQOTLYFGKRALRDNRIOLV 120
QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSLREKD 180
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QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240

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Db 241 IVCSVNHESLKADRSQRIEVLVYTTAMIRDPDHPHREGQKLLHCEGRGNPVPQOYL 300
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Db 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSSS 360
QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLIHRKGTLYLTHEAKGSDDAPDADTAIINAEGG 420
Db 361 STYHAIIGGIVAFIVFLLMLIFLGHYLIHRKGTLYLTHEAKGSDDAPDADTAIINAEGG 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 2
US-09-778-187b-8
; Sequence 8, Application US/09778187b
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187b
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 432
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187b-8

Query Match 100.0%; Score 2264; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLILLLLFACCAWAGGANLSQGYWQEQDLELGTAPLDEAISSTVWSSPDM 60
Db 1 MGAPASLILLLLFACCAWAGGANLSQGYWQEQDLELGTAPLDEAISSTVWSSPDM 60
QY 61 ASQDSQPWTSDETVVAGGTWVLCQVKHEDSSLOWNSPAQOTLYFGEKRALRDNRILQ 120
Db 61 ASQDSQPWTSDETVVAGGTWVLCQVKHEDSSLOWNSPAQOTLYFGEKRALRDNRILQ 120
QY 121 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTLVGIQPKPIITGYKSLREX 180
Db 121 TSTPHELSSISNVALADGEYTCSTFTMPVTRAKSLVTLVGIQPKPIITGYKSLREX 180
QY 181 TATLNCSSGKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKADRSQRIEVLVYTTAMIRDPDHPHREGQKLLHCEGRGNPVPQOYL 300
Db 241 IVCSVNHESLKADRSQRIEVLVYTTAMIRDPDHPHREGQKLLHCEGRGNPVPQOYL 300
QY 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSSS 360
Db 301 WEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSSS 360
QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLIHRKGTLYLTHEAKGSDDAPDADTAIINAEGG 420
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Db 361 STYHAIIGGIVAFIVFLLMLIFLGHYLIHRKGTLYLTHEAKGSDDAPDADTAIINAEGG 420
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RESULT 3
US-09-933-767-361
; Sequence 361, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
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; PRIOR APPLICATION NUMBER: 60/049,020
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; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
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; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
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; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
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; PRIOR APPLICATION NUMBER: 60/049,019
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; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 36.7009 Seconds
(without alignments)
3286.999 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

Sequence: 1 MGAPASLLLLLLLLFACWA.....AIINAEQSGGGDKKEYFI 432

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Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	432	9	US-09-778-510-2
2	2264	100.0	432	9	US-09-778-187B-8
3	2264	100.0	432	10	US-09-933-767-361
4	2264	100.0	432	14	US-10-161-572-49
5	2264	100.0	432	14	US-10-302-041-2
6	2059	90.9	398	9	US-09-745-763-102
7	2059	90.9	398	9	US-09-909-320-84
8	2059	90.9	398	9	US-09-909-088B-84
9	2059	90.9	398	9	US-09-905-291A-84
10	2059	90.9	398	9	US-09-778-510-6
11	2059	90.9	398	9	US-09-778-187B-10
12	2059	90.9	398	9	US-09-902-853-84
13	2059	90.9	398	9	US-09-907-824-84
14	2059	90.9	398	9	US-09-907-841-84
15	2059	90.9	398	10	US-09-904-011-84

16	2059	90.9	398	10	US-09-906-742-84	Sequence 84, Appl
17	2059	90.9	398	10	US-09-906-838-84	Sequence 84, Appl
18	2059	90.9	398	10	US-09-907-613-84	Sequence 84, Appl
19	2059	90.9	398	10	US-09-907-942-84	Sequence 84, Appl
20	2059	90.9	398	10	US-09-904-859-84	Sequence 84, Appl
21	2059	90.9	398	10	US-09-909-204-84	Sequence 84, Appl
22	2059	90.9	398	10	US-09-904-820-84	Sequence 84, Appl
23	2059	90.9	398	10	US-09-904-786-84	Sequence 84, Appl
24	2059	90.9	398	10	US-09-906-646-84	Sequence 84, Appl
25	2059	90.9	398	10	US-09-906-700-84	Sequence 84, Appl
26	2059	90.9	398	10	US-09-903-786-84	Sequence 84, Appl
27	2059	90.9	398	10	US-09-902-903-84	Sequence 84, Appl
28	2059	90.9	398	10	US-09-903-749A-84	Sequence 84, Appl
29	2059	90.9	398	10	US-09-904-119-84	Sequence 84, Appl
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33	2059	90.9	398	10	US-09-903-943-84	Sequence 84, Appl
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37	2059	90.9	398	10	US-09-903-520-84	Sequence 84, Appl
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39	2059	90.9	398	10	US-09-909-064-84	Sequence 84, Appl
40	2059	90.9	398	10	US-09-904-553-84	Sequence 84, Appl
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42	2059	90.9	398	10	US-09-905-088-84	Sequence 84, Appl
43	2059	90.9	398	10	US-09-907-575-84	Sequence 84, Appl
44	2059	90.9	398	10	US-09-905-075-84	Sequence 84, Appl
45	2059	90.9	398	10	US-09-902-759-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match 100.0%; Score 2264; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 1e-176;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGAPASLLLLLLLLFACWA	PGGANLSDGWQEO	DLGLTAPLDEA	ISSTVWSSPDL 60
DB	1	MGAPASLLLLLLLLFACWA	PGGANLSDGWQEO	DLGLTAPLDEA	ISSTVWSSPDL 60
QY	61	ASQDSQPWTSDET	VAGGTIVLKCQVKD	HEDSSLOWNPAQ	QOTLYFGEKRALRDNRIOLV 120
DB	61	ASQDSQPWTSDET	VAGGTIVLKCQVKD	HEDSSLOWNPAQ	QOTLYFGEKRALRDNRIOLV 120
QY	121	TSTPHELISISN	VALADEGYTCS	IFTMPVRTAKSL	VTVLGIPKPIITGYKSLREK 180
DB	121	TSTPHELISISN	VALADEGYTCS	IFTMPVRTAKSL	VTVLGIPKPIITGYKSLREK 180

Job time : 52.4442 secs

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2001-408281/43.
DR N-PSDB; AAS21417.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 348; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PMECs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 398 AA;
Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 3.5e-148;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYVQEQDLELGTILAPLDEAISITVWSSPDM 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQD----- 29
QY 61 ASQDSQPWTSDET VVAGT VVLKCOVKDHDSSLOWSNPAQOTLYFGKRALRDNRIQLV 120
DB 30 ---DSQPWTSDET VVAGT VVLKCOVKDHDSSLOWSNPAQOTLYFGKRALRDNRIQLV 86
QY 121 TSTPHELSISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSLREKD 180
DB 87 TSTPHELSISINVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSLREKD 146
QY 181 TATLNCQSSGSKPAARLTWRKQDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKQDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGADRSQRIEVLVYTPAMIRPDPPHPRGQKLLHCEGRGNVPQOYL 300
DB 207 IVCSVNHESLKGADRSQRIEVLVYTPAMIRPDPPHPRGQKLLHCEGRGNVPQOYL 266
QY 301 WEKESGVPPLKWTQESALIFPFLNKSDSGTGCTATSNMGSYKAYYTLNVNDPSVPSSS 360
DB 267 WEKESGVPPLKWTQESALIFPFLNKSDSGTGCTATSNMGSYKAYYTLNVNDPSVPSSS 326
QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLIIRHKGTYLTHEAKGSDPADADTAIINAE 420
DB 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLIIRHKGTYLTHEAKGSDPADADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2001-081051/09.
 DR N-PSDB; AAF72387.
 XX
 XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).
 XX
 XX Claim 1; Fig 32; 393pp; English.
 PS
 XX The present sequence is one of sixty one novel secreted and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful for treating skin
 CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosa. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping
 XX
 SQ Sequence 398 AA;

 Query Match 90.9%; Score 2059; DB 4; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

 QY 1 MGAPASLLLLLLFACCAAGGAGNLSQDGYWQBDLELGTAPLDEAISSTVWSSPDML 60
 DB 1 MGAPASLLLLLLFACCAAGGAGNLSQD----- 29

 QY 61 ASQDSQPTSDTETVAGGTVLKQVQKHEDSSLOWSNPAQOTLYFGCKEALRDNRILV 120
 DB 30 ---DSQPTSDTETVAGGTVLKQVQKHEDSSLOWSNPAQOTLYFGCKEALRDNRILV 86

 QY 121 TSTPHELISISNVALADEGYTCSTFTMPVTRAKSLVTLGIPQKDIITGYKSSIREKD 180
 DB 87 TSTPHELISISNVALADEGYTCSTFTMPVTRAKSLVTLGIPQKDIITGYKSSIREKD 146

 QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 DB 147 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206

 QY 241 IVCSNVHESLKGADRTSQRIEVLVYPTAMIRDPDHPREGQKLLHCEGRGNPVPQYL 300
 DB 207 IVCSNVHESLKGADRTSQRIEVLVYPTAMIRDPDHPREGQKLLHCEGRGNPVPQYL 266

 QY 301 WEKEGVPPLKMTQESALIFPPFLNKSDSGYGTCTATSNMGSKYKAYTYLNVNDESPVSS 360
 DB 267 WEKEGVPPLKMTQESALIFPPFLNKSDSGYGTCTATSNMGSKYKAYTYLNVNDESPVSS 326

 QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPADPATAINAE 420
 DB 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPADPATAINAE 386

QY 421 QSGGDDKKEYFI 432
 DB 337 QSGGDDKKEYFI 398

 RESULT 15
 AAU12345
 ID AAU12345 standard; protein; 398 AA.
 XX
 AC AAU12345;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO258 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US032678.
 XX
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 03-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX
 (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

```

Db      207  IVCSNVHESLKGADRSQSRIEVLVPTAMIRDPDPHPREGQKLLHCEGRGNVPVQQYL 266
QY      301  WEKEGSVPLKMTQESALIFPELNKSDSGYCTATSNMGSKAYYTLNVNDSFVPSSS 360
Db      267  WEKEGSVPLKMTQESALIFPELNKSDSGYCTATSNMGSKAYYTLNVNDSFVPSSS 326
QY      361  SYTHAIIIGGIVAFIVFVLLMLFLGHYLRHKGYTLTHEAKGSDDAPDADTAINAEGG 420
Db      327  SYTHAIIIGGIVAFIVFVLLMLFLGHYLRHKGYTLTHEAKGSDDAPDADTAINAEGG 386
QY      421  QSGGDDKKEYFI 432
Db      387  QSGGDDKKEYFI 398

RESULT 13
ADC78404
ID      ADC78404 standard; protein; 398 AA.
XX      ADC78404;
AC      AC
XX      XX
DT      01-JAN-2004 (first entry)
DE      Human PRO258 protein.
XX      XX
KW      antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW      neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW      neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW      antiarterioleclerotic; cardiast; antidiabetic; cerebroprotective;
KW      thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW      gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW      Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW      nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW      asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW      atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW      diabetes; stroke; gene therapy; transgenic; PRO; human.
XX      XX
OS      Homo sapiens.
XX      XX
PN      WO200015796-A2.
XX      XX
PD      23-MAR-2000.
XX      XX
PF      15-SEP-1999; 99WO-US021090.
XX      XX
PR      16-SEP-1998; 98WO-US019330.
XX      XX
PA      (GETH ) GENENTECH INC.
XX      XX
PI      Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI      Yuan J;
XX      XX
DR      WPI; 2000-271434/23.
DR      N-PSDB; ADC78403.
XX      XX
PT      Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT      homology, e.g. to growth and cancer-associated antigens.
XX      XX
PS      Claim 12; SEQ ID NO 84; 355pp; English.
XX      XX
CC      The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC      The polypeptides and polynucleotides of the invention may be useful as
CC      research tools and as therapeutics for treating enterocolitis, Zollinger-
CC      Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC      Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC      scarring and wound healing, nerve repair, thrombosis, bone and/or
CC      cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC      sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC      infertility, premature aging, AIDS, diabetes complications and stroke.
CC      The molecules may also be utilised during gene therapy procedures and
CC      transgenic animal production. The current sequence is that of the human
CC      PRO protein of the invention.

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XX      SQ      Sequence 398 AA;
Query Match      90.9%; Score 2059; DB 3; Length 398;
Best Local Similarity 92.1%; Pred. No. 3.5e-148;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
QY      1      MGAPASLALLLLFACCAWAGGANLSQGYQWQDLELGLTAPLDEALSSVTSWSPDML 60
Db      1      MGAPASLALLLLFACCAWAGGANLSQD----- 29
QY      61      ASQDSQPTSDETVAGGTIVLKCVKDHEDSSLOWNSPAQOTLYFGEKRALRDNRIOLV 120
Db      30      ---DSQPTSDETVAGGTIVLKCVKDHEDSSLOWNSPAQOTLYFGEKRALRDNRIOLV 86
QY      121     TSTPHLSISINVALADEGEYTCSTFTMPVTRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db      87      TSTPHLSISINVALADEGEYTCSTFTMPVTRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY      181     TATLNCOSSGSKPAARLTWRKGDQELHCEPTRIOEDPNGKTFVSSSVTFQVTRDDGAS 240
Db      147     TATLNCOSSGSKPAARLTWRKGDQELHCEPTRIOEDPNGKTFVSSSVTFQVTRDDGAS 206
QY      241     IVCSNVHESLKGADRSQSRIEVLVPTAMIRDPDPHPREGQKLLHCEGRGNVPVQQYL 300
Db      207     IVCSNVHESLKGADRSQSRIEVLVPTAMIRDPDPHPREGQKLLHCEGRGNVPVQQYL 266
QY      301     WEKEGSVPLKMTQESALIFPELNKSDSGYCTATSNMGSKAYYTLNVNDSFVPSSS 360
Db      267     WEKEGSVPLKMTQESALIFPELNKSDSGYCTATSNMGSKAYYTLNVNDSFVPSSS 326
QY      361     SYTHAIIIGGIVAFIVFVLLMLFLGHYLRHKGYTLTHEAKGSDDAPDADTAINAEGG 420
Db      327     SYTHAIIIGGIVAFIVFVLLMLFLGHYLRHKGYTLTHEAKGSDDAPDADTAINAEGG 386
QY      421     QSGGDDKKEYFI 432
Db      387     QSGGDDKKEYFI 398

RESULT 14
AAB80226
ID      AAB80226 standard; protein; 398 AA.
XX      AC
XX      AAB80226;
XX      XX
DT      24-APR-2001 (first entry)
XX      DE
XX      Human PRO258 protein.
XX      XX
KW      Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW      antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiast;
KW      antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW      antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW      ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW      ischaemia; inflammation.
XX      OS
XX      Homo sapiens.
XX      XX
PN      WO200104311-A1.
XX      XX
PD      18-JAN-2001.
XX      XX
PF      22-FEB-2000; 2000WO-US004414.
XX      XX
PR      07-JUL-1999; 99US-0143048P.
PR      26-JUL-1999; 99US-0145698P.
PR      28-JUL-1999; 99US-0146222P.
PR      08-SEP-1999; 99WO-US020594.
PR      13-SEP-1999; 99WO-US020944.
PR      15-SEP-1999; 99WO-US021090.
PR      15-SEP-1999; 99WO-US021547.
PR      05-OCT-1999; 99WO-US023089.

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PT Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
 PT costimulatory molecules for therapeutics against infections, autoimmune
 XX diseases and inflammation.
 XX
 PS Claim 8; Page 47-48; 57pp; English.
 XX
 CC The present sequence represents the short extracellular form of human B7-
 CC 1 (CD80). B7-1 is a T-cell costimulatory molecule that is found on the
 CC surface of antigen presenting cells (APCs). CD28 and CTLA4 are its T cell
 CC surface receptors. B7-1 interacts with CD28 to signal cytokine
 CC production, cell proliferation, and the generation of effector and memory
 CC T cells. Disorders mediated by interaction of B7-1 and its binding
 CC partner, such as infections, autoimmune diseases and inflammation, are
 CC treated by administering B7L-1 to the disordered mammal. B7L-1
 CC polypeptides are useful to separate cells expressing a protein to which
 CC it binds and to measure the biological activity of LDCAM polypeptides.
 CC They can also be used as reagents for conducting quality assurance
 CC studies e.g., to monitor shelf life and stability of proteins to which it
 CC binds, and as carriers for delivering agents attached to cells bearing
 CC its counter structure, LDCAM or other cell receptors. They are also
 CC useful as a research tool for studying T-cell signalling and
 CC proliferation. They are employed in in vitro assays for detecting
 CC interactions of LDCAM with T-cell receptors. Diagnostic and therapeutic
 CC agents, such as drugs, toxins, radionuclides, chromophores, and enzymes
 CC which catalyze a colorimetric or fluorometric reaction, may be attached
 CC to a B7L-1 polypeptide, e.g. nitrogen mustards are attached to the B7L-1
 CC and used to treat various forms of cancer
 XX
 SQ Sequence 398 AA;

Query Match 90.9%; Score 2059; DB 3; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQDLEGLTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQDLEGLTAPLDEAISTVWSSPDML 29
 QY 61 ASQDSQPWTSDETIVVAGGTWVLKQVKDHEDSSLOWSNPAQOTLYFGEKALRDNRIQLV 120
 Db 30 ---DSQPWTSDETIVVAGGTWVLKQVKDHEDSSLOWSNPAQOTLYFGEKALRDNRIQLV 86
 QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
 Db 87 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
 QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206
 QY 241 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 300
 Db 207 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 266
 QY 301 WEKEGVPPLKMTQESALIPFPFLNKSDSGTYGCTATSNMGSKYAYTVLNVDPSPVSS 360
 Db 267 WEKEGVPPLKMTQESALIPFPFLNKSDSGTYGCTATSNMGSKYAYTVLNVDPSPVSS 326
 QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPADTAIINAEAG 420
 Db 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPADTAIINAEAG 386
 QY 421 QSGGDDKKEYFI 432
 Db 387 QSGGDDKKEYFI 398

RESULT 12

AAV45095

ID AAY45095 standard; protein; 398 AA.

XX AAY45095;

AC AAY45095;

XX

DT 31-MAY-2000 (first entry)
 XX Human LDCAM binding protein, B7L-1 short form.
 DE
 XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-L1;
 KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
 KW biological activity; quality control reagent; treatment; inflammation;
 KW immune system disorder; autoimmune; viral infection; infectious disease;
 KW organ transplant rejection; bone marrow; modulator; immune response.
 XX
 OS Homo sapiens.
 XX
 PN WO200008158-A2.
 XX
 PD 17-FEB-2000.
 XX
 PF 05-AUG-1999; 99WO-US017905.
 XX
 PR 07-AUG-1998; 98US-0095672P.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Baum PE, Fanslow WC;
 PI
 XX WPI; 2000-205712/18.
 DR
 XX N-PSDB; AAZ50887.
 PT
 XX Novel molecules designated LDCAM are capable of altering or modulating T
 PT cell function.

Disclosure; Page 53-54; 44pp; English.

The present amino acid sequence is the human LDCAM (lymphoid derived
 dendritic cell adhesion molecule) binding protein, B7L-1 short form. B7L
 -1 has sequence similarity to adhesion molecule, B7-1. B7L-1 and LDCAM
 display homology within their intracellular domain, found on many of the
 same cell types and their cell-bound forms deliver similar signals when
 engaged and are termed as co-receptors or counter structures. LDCAM
 polypeptides interacts with T cell surface molecules to alter signalling
 and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM
 binding protein and increases natural killer (NK) cell populations. It
 may be used to measure the biological activity and as quality control
 reagents of LDCAM binding proteins. LDCAM may be used for treating
 disorders associated with malfunctioning of immune system, inflammation,
 autoimmune disorders, viral infected cells, infectious diseases and for
 killing tumour cells. They are also useful for prevention or reducing the
 effect of organ and bone marrow transplant rejection and for modulating T
 cell immune responses. LDCAM polypeptides may also be used as carriers
 for delivering agents attached to T cells or cells bearing B7L-1

Sequence 398 AA;

Query Match 90.9%; Score 2059; DB 3; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQDLEGLTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAALLLLLLFACCCWAPGGANLSDGQVWQDLEGLTAPLDEAISTVWSSPDML 29
 QY 61 ASQDSQPWTSDETIVVAGGTWVLKQVKDHEDSSLOWSNPAQOTLYFGEKALRDNRIQLV 120
 Db 30 ---DSQPWTSDETIVVAGGTWVLKQVKDHEDSSLOWSNPAQOTLYFGEKALRDNRIQLV 86
 QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 180
 Db 87 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLRKD 146
 QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206
 QY 241 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQQYL 300

Db	327	STYHALGGIVAFIVFLLMLILFGLHYLRHKGYLT	HEAKGSDPADPADTAI	NAEGG	398
Qy	421	QSGGDDKKEYFI	432		
Db	387	QSGGDDKKEYFI	398		
RESULT 10					
AAAY94403					
ID	AAAY944403	standard; protein; 398	AA		
XX	AC	AAAY94403;			
XX	DT	11-SEP-2000 (first entry)			
XX	DE	Human ACAM cellular adhesion molecule encoded by cDNA clone ACAM#4.			
XX	KW	Human; cellular adhesion molecule; ACAM; nontropic; antiepileptic;			
KW	KW	neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;			
KW	KW	dementia; epilepsy; schizophrenia; peripheral nerve injury;			
KW	KW	diabetic neuropathy.			
XX	OS	Homo sapiens.			
XX	Key	Location/Qualifiers			
FH	Peptide	1..24			
FT	Protein	/label= Signal_peptide			
FT	FT	25..398			
FT	FT	/label= ACAM			
XX	PN	WO200032633-Al.			
XX	PD	08-JUN-2000.			
XX	PF	02-DEC-1999; 99WO-US028878.			
XX	PR	02-DEC-1998; 98US-00203462.			
XX	PA	(ICOS-) ICOS CORP.			
XX	PI	Hoekstra DM, Loughney K, Stauton DE, Vazeux R;			
XX	PI	WPI: 2000-422952/36.			
DR	DR	N-PSDB; AAY94403.			
XX	PT	Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful			
PT	PT	for diagnosing, preventing and treating diseases associated with ACAM			
PT	PT	expression and activity, e.g. epilepsy and schizophrenia.			
XX	PS	Claim 5; Page 149-150; 187pp; English.			
XX	CC	The present sequence is a novel adhesion molecule, designated ACAM. The			
CC	CC	full-length nucleotide sequence was identified in clone ACAM#4 of a human			
CC	CC	fetal brain library. The polypeptide is 100% homologous to the			
CC	CC	polypeptide encoded by clone ACAM#6 (AAA30423) from the same library			
CC	CC	except that it contains a 34 amino acid deletion. It is believed to			
CC	CC	correspond to an alternative form of ACAM. The nucleotide sequence and			
CC	CC	the protein it encodes may be used in the prevention, treatment and			
CC	CC	diagnosis of diseases associated with inappropriate ACAM expression and			
CC	CC	activity such as dementia, epilepsy, schizophrenia, peripheral nerve			
CC	CC	injuries and diabetic neuropathies. They may be used to rectify mutations			
CC	CC	or deletions in a patient's genome that affect the activity of ACAM or to			
CC	CC	supplement insufficient ACAM production in a patient. The nucleotide			
CC	CC	sequence may be integrated into an expression vector and inserted into a			
CC	CC	host cell for protein expression in vitro or in vivo. Conversely,			
CC	CC	antisense nucleic acid molecules may be administered to down-regulate			
CC	CC	ACAM expression. The nucleotide sequence may also be used as a DNA probe			
CC	CC	in diagnostic assays (e.g. PCR) to detect and quantitate the presence of			
CC	CC	similar nucleic acid sequences in samples, and hence determine which			
CC	CC	patients may be in need of restorative therapy. ACAM polypeptides may be			
CC	CC	used as antigens in the production of antibodies against ACAM and in			
CC	CC	assays to identify modulators (agonists and antagonists) of ACAM			

QY 421 QSGGDDKKEYFI 432
 Db 387 QSGGDDKKEYFI 398
 RESULT 9
 AAY13358
 ID AAY13358 standard; protein; 398 AA.
 XX AC AAY13358;
 XX DT 25-JUN-1999 (first entry)
 XX DE Amino acid sequence of protein PRO258.
 XX KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophica areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX OS Homo sapiens.
 XX PN WO9914328-A2.
 XX PD 25-MAR-1999.
 XX PF 16-SEP-1998; 98WO-US019330.
 XX PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063341P.
 PR 28-OCT-1997; 97US-0063342P.
 PR 28-OCT-1997; 97US-0063344P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 29-OCT-1997; 97US-0063356P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 31-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 18-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 XX (GETH) GENENTECH INC.
 XX FI Wood WZ, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 XX DR WPI; 1999-229533/19.
 XX DR N-PSDB; AAX52229.
 XX PT New isolated human genes and polypeptides used in, e.g. treatment of
 XX ST Gastrointestinal ulceration.
 XX PS Claim 12; Fig 32; 320pp; English.
 XX CC AAY13344-403 represent secreted and transmembrane human proteins. The
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 CC encoded polypeptides have specific uses based on their homology to known
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 CC with the preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
 CC and development, diseases related to growth or survival of nerve cells
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophica areata; PRO269 can
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX SQ Sequence 398 AA;
 Query Match 90.9%; Score 2059; DB 2; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAASLLLLLLLLFACCCWAPGGANLSQDGYWQEQDLELGTLPALDEAISTVWSSPDML 60
 Db 1 MGAPAAASLLLLLLLLFACCCWAPGGANLSQD-----29
 QY 61 ASQDSQPWTSDETVVAGGTIVLKQVQKHEDSSLOWSNPAQOTLYFGEKRALDRNRQIV 120
 Db 30 ---DSQPWTSDETVVAGGTIVLKQVQKHEDSSLOWSNPAQOTLYFGEKRALDRNRQIV 86
 QY 121 TSTPHELSTISINVALADEGEYTCISIFTPMPTAKSLVTLGIPQKPIITGVKSSIREKD 180
 Db 87 TSTPHELSTISINVALADEGEYTCISIFTPMPTAKSLVTLGIPQKPIITGVKSSIREKD 146
 QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTFVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTFVSSSVTFQVTRDDGAS 206
 QY 241 IVCSVNHESLKADSTSORIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQYVL 300
 Db 207 IVCSVNHESLKADSTSORIEVLYTPTAMIRPDPPHREGQKLLHCEGRGNPVPQYVL 266
 QY 301 WEKGSVPPLKMTQESALIFPFLNKSDSGTGCTATSNMGYSKAYTILNVNDPSPVSSS 360
 Db 267 WEKGSVPPLKMTQESALIFPFLNKSDSGTGCTATSNMGYSKAYTILNVNDPSPVSSS 326
 QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLIHRKGTLYLTHAKGSDADPADADTAIINAE 420

CC The present sequence represents a secreted protein. The nucleic acid
 CC sequence is isolated from a human adult testes cDNA library using probe
 CC AAV63200. The polypeptide may have biological activities such as e.g.
 CC nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity, haemostatic
 CC activin/inhibin activity, chemotactic/chemokinetic activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity or other activities. (Updated on 25-MAR-2003 to correct PR
 CC field.)
 CC
 XX Sequence 398 AA;

Query Match 90.9%; Score 2059; DB 2; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAALLLLLLFACCCWAPGGANLSQDGYWQDLELGLTAPLDEAISSTVWSSPDML 60
 DB 1 MGAPAAALLLLLLFACCCWAPGGANLSQD----- 29
 QY 61 ASQDSQPTSDTETVAGGTVVLKQVXKHEDSSLOWNPAAQOTLYFGKRALRDNRIQLV 120
 DB 30 ---DSQPTSDTETVAGGTVVLKQVXKHEDSSLOWNPAAQOTLYFGKRALRDNRIQLV 86
 QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
 DB 87 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
 QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 DB 147 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206
 QY 241 IVCSNVHESLKGADRSQSRIEVLVYTPAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 300
 DB 207 IVCSNVHESLKGADRSQSRIEVLVYTPAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 266
 QY 301 WEKESVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDSPSPSS 360
 DB 267 WEKESVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDSPSPSS 326
 QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAGSDDDAPDADTAIINAEGG 420
 DB 327 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAGSDDDAPDADTAIINAEGG 386
 QY 421 QSGDDKKKEYFI 432
 DB 387 QSGDDKKKEYFI 398

RESULT 8
 AAY29592
 ID AAY29592 standard; protein; 398 AA.
 AC AAY29592;
 DT 14-OCT-1999 (first entry)
 XX Human MBGP1 protein.
 DE Human; MBGP1; therapy; diagnosis; immunoglobulin; multiple sclerosis;
 KW cancer; neuronal disorder; CNS disorder; developmental disorder;
 KW spinal injury; degenerative condition; viral infection; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN EP939124-A2.
 PD 01-SEP-1999.
 XX
 PF 27-OCT-1998; 98EP-00203617.
 XX
 PR 24-FEB-1998; 98GB-00003952.

PR 12-AUG-1998; 98GB-00017588.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Duckworth DM, Burgess NA;
 XX
 DR WPI; 1999-480841/41.
 DR N-PSDB; AAZ08540.
 XX
 PT New immunoglobulin superfamily member, useful for diagnosing and treating
 PT multiple sclerosis and cancer.

Claim 4; Page 17-18; 21pp; English.

XX The present sequence represents human MBGP1, which is a member of the
 XX immunoglobulin superfamily. MBGP1 may be used to screen for its agonists
 XX or antagonists by contacting MBGP1 with the candidate compound and
 XX detecting any alteration in activity of MBGP1 or in a label attached to
 XX the candidate. Alternatively the effect of a candidate agonist or
 XX antagonist compound on the production of mRNA encoding MBGP1 may be
 XX detected using an ELISA assay. Diseases or conditions arising from
 XX altered expression or activity of MBGP1 may be diagnosed by detecting
 XX MBGP1 in a sample from a patient or detecting a mutation in the
 XX polynucleotide encoding MBGP1 (i) in the genome of a patient. These
 XX diseases or conditions include neurological disorders such as multiple
 XX sclerosis, CNS disorders, developmental disorders, spinal injury,
 XX degenerative conditions, cancer and viral infections. Detection of (i)
 XX may be used for chromosome mapping and tissue localization. MBGP1 and (i)
 XX may be administered to patients as vaccines or as part of a gene therapy
 XX regime respectively, to treat the diseases and conditions listed above.
 XX Antibodies against MBGP1 may be used to isolate or identify clones
 XX expressing MBGP1 or to purify MBGP1 by affinity chromatography. MBGP1 may
 XX also be used to identify molecules which interact with it in or on the
 XX surface of cells. Antagonists of MBGP1 may be administered to patients
 XX suffering from the above diseases or conditions related to increased
 XX expression or activity of MBGP1. Agonists of MBGP1 may similarly be used
 XX in cases of diseases or conditions related to decreased expression or
 XX activity of MBGP1

SQ Sequence 398 AA;

Query Match 90.9%; Score 2059; DB 2; Length 398;
 Best Local Similarity 92.1%; Pred. No. 3.5e-148;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAALLLLLLFACCCWAPGGANLSQDGYWQDLELGLTAPLDEAISSTVWSSPDML 60
 DB 1 MGAPAAALLLLLLFACCCWAPGGANLSQD----- 29
 QY 61 ASQDSQPTSDTETVAGGTVVLKQVXKHEDSSLOWNPAAQOTLYFGKRALRDNRIQLV 120
 DB 30 ---DSQPTSDTETVAGGTVVLKQVXKHEDSSLOWNPAAQOTLYFGKRALRDNRIQLV 86
 QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
 DB 87 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
 QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 DB 147 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 206
 QY 241 IVCSNVHESLKGADRSQSRIEVLVYTPAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 300
 DB 207 IVCSNVHESLKGADRSQSRIEVLVYTPAMIRPDPPHREGQKLLHCEGRGNVPVQOYL 266
 QY 301 WEKESVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDSPSPSS 360
 DB 267 WEKESVPLKMTQESALIPFLNKSQSGTYGCTATSNMGSKYKAYITLVNNDSPSPSS 326
 QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAGSDDDAPDADTAIINAEGG 420
 DB 327 STYHAIIGGIVAFIVFLLMLIFLGHYLRHKGTYLTHEAGSDDDAPDADTAIINAEGG 386

QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREKD 180
 DB 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREKD 180
 QY 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGAS 240
 DB 181 TATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGAS 240
 QY 241 IVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNVPVPOYL 300
 DB 241 IVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNVPVPOYL 300
 QY 301 WEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 360
 DB 301 WEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 360
 QY 361 STYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKGYLTTHAEKGSDDADPADTALINAE 420
 DB 361 STYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKGYLTTHAEKGSDDADPADTALINAE 420
 QY 421 QSGGDDKKEYFI 432
 DB 421 QSGGDDKKEYFI 432

RESULT 6
 AA53272 ID AA53272 standard; protein; 433 AA.
 XX AC AA53272;
 XX XX
 DT 21-JUL-2000 (first entry)
 DE Human Beat-like 1 (BL1) protein sequence.
 XX XX
 KW Human; Beat-like 1; BL1; nervous system.
 OS Homo sapiens.
 XX CN1242376-A.
 PD 26-JAN-2000.
 XX XX
 PF 27-JUL-1999; 99CN-00111018.
 XX 27-JUL-1999; 99CN-00111018.
 XX (BASI-) BASIC MEDICAL SCI RES INST CHINESE ACAD.
 PA Zhang B, Yuan J, Zhou Y;
 PI WPI; 2000-340013/30.
 DR N-PSDB; AAA13653.
 XX Human gene expressed in nerve tissue for studying tissue function.
 PT Disclosure; Fig 2; 14pp; Chinese.
 PS The present invention relates to a new specific expression gene, Beat-
 CC like 1 (BL1), from the human nervous system. BL1 is a nervous adhesion
 CC molecule and its specific expression can possess important action in
 CC maintenance of physiological function of the nervous system and
 CC pathogenic processes of some nervous system diseases. The present
 CC sequence represents the human BL1 given in the present invention
 XX SQ Sequence 433 AA;
 Query Match 99.5%; Score 2253.5; DB 3; Length 433;
 Best Local Similarity 99.8%; Pred. No. 6.2e-163;
 Matches 432; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MGAPAAALLLLLLFACCAWAPGANLSQGYWQEDLELGLTAPLDEAISSTVMSSPDML 60
 |||||

DB 1 MGAPAAALLLLLLFACCAWAPGANLSQGYWQEDLELGLTAPLDEAISSTVMSSPDML 60
 QY 61 ASQDSQPTSDTETVAGGTVVLKQVKDHEDSSLOWNPAQOOLYFGEKALDRNRIOLV 120
 DB 61 ASQDSQPTSDTETVAGGTVVLKQVKDHEDSSLOWNPAQOOLYFGEKALDRNRIOLV 120
 QY 121 TSTPHELISISINVALAD-EGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREK 179
 DB 121 TSTPHELISISINVALADEGEYTCISFTMPVTRAKSLVTLVGIPOKPIITGYKSSIREK 180
 QY 180 DTATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGA 239
 DB 180 DTATLNCSSGSKPAARLTWRKQDELHGEPTRIQEDPENGKTFVSSSVTFQVTRDDGA 240
 QY 240 SIIVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNVPVPOY 299
 DB 240 SIIVCSVNHESLKGDARSTSORIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNVPVPOY 300
 QY 300 LWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 359
 DB 300 LWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSKYKAYTTLNVNDSPVPSS 360
 QY 360 SSTYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKGYLTTHAEKGSDDADPADTALINAE 419
 DB 360 SSTYHAIIGGIVAFIVFLLMLIFLGHYLIIRHKGYLTTHAEKGSDDADPADTALINAE 420
 QY 420 GQSGGDDKKEYFI 432
 DB 420 GQSGGDDKKEYFI 433

RESULT 7
 AAW80405 ID AAW80405 standard; protein; 398 AA.
 XX AC AAW80405;
 XX XX
 DT 25-MAR-2003 (revised)
 DT 13-JAN-1999 (first entry)
 XX XX
 DE A secreted protein encoded by clone crll62_25.
 XX KW Secreted protein; immune stimulating; suppressing;
 KW haematopoiesis regulating activity; tissue growth activity; activin;
 KW inhibin activity; chemotactic; chemokinetic activity; haemostatic;
 KW thrombolytic activity; anti-inflammatory activity; cadherin;
 KW tumour invasion suppressor activity; tumour inhibition activity.
 XX OS Homo sapiens.
 XX WO9844113-A1.
 XX PD 08-OCT-1998.
 XX PF 27-MAR-1998; 98WO-US006176.
 XX PR 28-MAR-1997; 97US-00823330.
 XX PR 25-MAR-1998; 98US-00047661.
 XX (GEMY) GENETICS INST INC.
 XX Jacobs K, McCooy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX WPI: 1998-542703/46.
 DR N-PSDB; AAV63189.
 XX New isolated polynucleotide(s) and secreted proteins - are obtained from
 PT human cDNA libraries prepared from adult testes, foetal brain, adult
 PT brain, adult blood and placenta.
 XX PS Claim 13; Page 70-71; 124pp; English.

XX PI Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
 PI Florence C, Hu J, Li Y, Kwaw H, Fischer CL, Ferrie AM, Fan P;
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z;
 PI Greene JM;
 DR WPI; 2001-625724/72.
 DR N-PSDB; ABA83306.
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 XX Claim 11; Page 1142-1143; 1533pp; English.
 XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;
 CC neuroprotective; neurotropic; anticonvulsant; antialzheimers; vascular;
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention
 XX SQ Sequence 432 AA;
 Query Match 100.0%; Score 2264; DB 4; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAALLLLLLFACCAWPGGANLSQDGYWQDLELGLTAPLDEAISTVWSSPDL 60
 DB 1 MGAPAAALLLLLLFACCAWPGGANLSQDGYWQDLELGLTAPLDEAISTVWSSPDL 60
 QY 61 ASQDSQPWTSDETAVAGTGVVLCQVQKDHEDSSLOWNPAQQTLYFGEKRALRNRIOLV 120
 DB 61 ASQDSQPWTSDETAVAGTGVVLCQVQKDHEDSSLOWNPAQQTLYFGEKRALRNRIOLV 120
 QY 121 TSTPHELISISNVALADEGEYTCISITMPVRTAKSLTVVLGIPQKPIITGYKSSUREKD 180
 DB 121 TSTPHELISISNVALADEGEYTCISITMPVRTAKSLTVVLGIPQKPIITGYKSSUREKD 180
 QY 181 TATLNCSSGSKPAARLTWRKGDQLHGEPTRIQEDPNGKFTVSSVTVQVTRDDGAS 240
 DB 181 TATLNCSSGSKPAARLTWRKGDQLHGEPTRIQEDPNGKFTVSSVTVQVTRDDGAS 240
 QY 241 IVCSVNHELKGDARSQRIEVLVYTPAMTRPPPHREGOKLLHCEGRGNVPQOYL 300
 DB 241 IVCSVNHELKGDARSQRIEVLVYTPAMTRPPPHREGOKLLHCEGRGNVPQOYL 300
 QY 301 WEKESGVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYTYTLNVNDSPVPSS 360
 DB 301 WEKESGVPPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSYKAYTYTLNVNDSPVPSS 360
 QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLRHKGTYYLTHRAKGSDDAPDADTAIINAE 420
 DB 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLRHKGTYYLTHRAKGSDDAPDADTAIINAE 420
 QY 421 QSGGDDKKEYFI 432
 |||||

DB 421 QSGGDDKKEYFI 432
 RESULT 5
 ABO20226
 ID ABO20226 standard; protein; 432 AA.
 XX AC ABO20226;
 XX AC ABO20226;
 DT 13-AUG-2003 (first entry)
 XX Human IG gene related protein SEQ ID No 49.
 DE Breast cancer; p53 pathway modulating agent; IG; colon cancer;
 XX kidney cancer; lung cancer; ovary cancer; human.
 KW Homo sapiens.
 OS WO200259040-A2.
 XX 12-DEC-2002.
 PD 03-JUN-2002; 2002WO-US017313.
 PF 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 22-OCT-2001; 2001US-0338733P.
 PR 15-FEB-2002; 2002US-0357253P.
 PR 15-FEB-2002; 2002US-0357600P.
 XX (EXEL-) EXELIXIS INC.
 PA Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 PI Lioubin MN;
 XX WPI; 2003-148660/14.
 DR Identifying a candidate p53 pathway modulators that are useful as targets
 XX for therapeutics or for diagnosing cancers associated with defective p53
 PT function, by providing an assay system having a purified IG polypeptide
 PT or nucleic acid.
 XX Claim 13; Page 214-216; 248pp; English.
 PS The invention relates to a novel method for identifying a candidate p53
 CC pathway modulating agent. The method comprises providing an assay system
 CC having a purified IG polypeptide or nucleic acid, or their functionally
 CC active fragment or derivative. The method is useful for identifying
 CC modulators of the p53 pathway, particularly for identifying agents for
 CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
 CC cancer or cancer of the ovary) associated with defective p53 function.
 CC The identified modulators are useful as targets for novel therapeutics.
 CC The method is also useful for diagnosing disorders associated with
 CC defective p53 function. The IG proteins or nucleic acids are useful as
 CC modifiers of the p53 pathway, and as therapeutic targets for disorders
 CC associated with defective p53 function. This sequence represents a human
 CC protein relating to the human IG genes used in the assay for identifying
 CC modulators of the p53 pathway of the invention
 XX SQ Sequence 432 AA;
 Query Match 100.0%; Score 2264; DB 6; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAALLLLLLFACCAWPGGANLSQDGYWQDLELGLTAPLDEAISTVWSSPDL 60
 DB 1 MGAPAAALLLLLLFACCAWPGGANLSQDGYWQDLELGLTAPLDEAISTVWSSPDL 60
 QY 61 ASQDSQPWTSDETAVAGTGVVLCQVQKDHEDSSLOWNPAQQTLYFGEKRALRNRIOLV 120
 DB 61 ASQDSQPWTSDETAVAGTGVVLCQVQKDHEDSSLOWNPAQQTLYFGEKRALRNRIOLV 120

||||| 241 IVCSVNHESLKADRSQSRLEVIYTPAMIRPPPHREGQKLLHCEGRGNFVPOQYL 300
Db
Qy 301 WEKEGVSPPPLKMTQESALIFPFLNKSDSGTGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Db 301 WEKEGVSPPPLKMTQESALIFPFLNKSDSGTGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Qy 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Db 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Qy 421 QSGGDDKXEYFI 432
Db 421 QSGGDDKXEYFI 432

RESULT 3
AAY45094
ID AAY45094 standard; protein; 432 AA.
XX AC AAY45094;
XX DT
XX 31-MAY-2000 (first entry)
XX DE Human LDCAM binding protein, B7L-1 long form.
XX KW Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
KW biological activity; quality control reagent; treatment; inflammation;
KW immune system disorder; autoimmune; viral infection; infectious disease;
KW organ transplant rejection; bone marrow; modulator; immune response.
XX OS Homo sapiens.
XX PN W0200008158-A2.
XX PD 17-FEB-2000.
XX PF 05-AUG-1999; 99WO-US017905.
XX PR 07-AUG-1998; 98US-0095672P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC;
XX DR WPI; 2000-205712/18.
XX DR N-PSDB; AAZ50886.
XX Novel molecules designated LDCAM are capable of altering or modulating T cell function.
XX Disclosure; Page 50-51; 44pp; English.
XX The present amino acid sequence is the human LDCAM (lymphoid derived dendritic cell adhesion molecule) binding protein, B7L-1 long form. B7L-1 has sequence similarity to adhesion molecule, B7-1. B7L-1 and LDCAM display homology within their intracellular domain, found on many of the same cell types and their cell-bound forms deliver similar signals when engaged and are termed as co-receptors or counter structures. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7L-1

Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 9,9e-164; Indels 0; Gaps 0;
Matches 432; Conservative 0; Mismatches 0;
Qy 1 MGAPAAALLLLLFACCWAPGGANLSQDGYWQBDLELGTALFLDEAISSTVWSSPDM 60
Db 1 MGAPAAALLLLLFACCWAPGGANLSQDGYWQBDLELGTALFLDEAISSTVWSSPDM 60
Qy 61 ASQDSQPTSDTETVAGTIVLKCQVXKHEDSSLOWNPAQOTLYFGKKALRNRIQLV 120
Db 61 ASQDSQPTSDTETVAGTIVLKCQVXKHEDSSLOWNPAQOTLYFGKKALRNRIQLV 120
Qy 121 TSTPHELISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLEKD 180
Db 121 TSTPHELISISNVALADEGEYTCISFTMPVTRAKSLVTVLGIPOKPIITGYKSSLEKD 180
Qy 181 TATLNCOSGSKPAARLTWRKQDQLHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Db 181 TATLNCOSGSKPAARLTWRKQDQLHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
Qy 241 IVCSVNHESLKADRSQSRLEVIYTPAMIRPPPHREGQKLLHCEGRGNFVPOQYL 300
Db 241 IVCSVNHESLKADRSQSRLEVIYTPAMIRPPPHREGQKLLHCEGRGNFVPOQYL 300
Qy 301 WEKEGVSPPPLKMTQESALIFPFLNKSDSGTGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Db 301 WEKEGVSPPPLKMTQESALIFPFLNKSDSGTGCTATSNMGSYKAYITLVNDPSPVPSSS 360
Qy 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Db 361 STYHAIIGGIVAFIVFLLIMLIFLGHVLIIRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Qy 421 QSGGDDKXEYFI 432
Db 421 QSGGDDKXEYFI 432

RESULT 4
ABB50413
ID ABB50413 standard; protein; 432 AA.
XX AC ABB50413;
XX DT
XX 07-FEB-2002 (first entry)
XX Human secreted protein encoded by gene 113 SEQ ID NO:361.
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
XX cytostatic; cardiac; anti-angiogenic; ophthalmological;
XX neuroprotective; nontropic; anticonvulsant; antialzheimers; vulnary;
XX antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
XX multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
XX human immunodeficiency virus; hyperproliferative disorder; wound healing;
XX Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
XX Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
XX corneal graft neovascularisation; diabetic retinopathy; regeneration;
XX neurological disorder; Huntington's chorea; Alzheimer's disease;
XX Parkinson's disease; infectious disease; chromosome 1.
XX Homo sapiens.
XX OS
XX W0200162891-A2.
XX 30-AUG-2001.
XX 21-FEB-2001; 2001WO-US005614.
XX 24-FEB-2000; 2000US-0184836P.
XX 29-MAR-2000; 2000US-0193170P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA

CC dementia, epilepsy, schizophrenia, peripheral nerve injuries and diabetic
 CC neuropathies. They may be used to rectify mutations or deletions in a
 CC patient's genome that affect the activity of ACAM or to supplement
 CC insufficient ACAM production in a patient. The nucleotide sequence may be
 CC integrated into an expression vector and inserted into a host cell for
 CC protein expression in vitro or in vivo. Conversely, antisense nucleic
 CC acid molecules may be administered to down-regulate ACAM expression. The
 CC nucleotide sequence may also be used as a DNA probe in diagnostic assays
 CC (e.g. PCR) to detect and quantitate the presence of similar nucleic acid
 CC sequences in samples, and hence determine which patients may be in need
 CC of restorative therapy. ACAM polypeptides may be used as antigens in the
 CC production of antibodies against ACAM and in assays to identify
 CC modulators (agonists and antagonists) of ACAM expression and activity
 XX
 XX
 XX Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 3; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 QY 61 ASQDSQPWTSDETVAAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIOIV 120
 Db 61 ASQDSQPWTSDETVAAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIOIV 120
 QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSLREKD 180
 Db 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSLREKD 180
 QY 181 TATLNCQSSGSKPAARLTWRKGDDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 Db 181 TATLNCQSSGSKPAARLTWRKGDDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMRDPDPHPRGQKLLHCEGRGNVPVQOYL 300
 Db 241 IVCSNVHESLKGADRSQRIEVLVYPTAMRDPDPHPRGQKLLHCEGRGNVPVQOYL 300
 QY 301 WEKEGVPPLKMTQESALIPFLNKSQSGTYGCTATSNMGSYKAYVTLNVNDSPVPSSS 360
 Db 301 WEKEGVPPLKMTQESALIPFLNKSQSGTYGCTATSNMGSYKAYVTLNVNDSPVPSSS 360
 QY 361 STYHAIIGGIVATVFLMLLFLPHYLIRHKGTVLTHEAKGSDDAPDADTAIINAEKG 420
 Db 361 STYHAIIGGIVATVFLMLLFLPHYLIRHKGTVLTHEAKGSDDAPDADTAIINAEKG 420
 QY 421 QSGGDDKKEYFI 432
 Db 421 QSGGDDKKEYFI 432

RESULT 2
 AAY69286
 ID AAY69286 standard; protein; 432 AA.
 XX
 AC AAY69286;
 DT 19-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of long extracellular form of human B7-1 (CD80).
 KW Long form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
 KW CD28; CTLA4; T cell surface receptor; cytokine production;
 KW cell proliferation; T cell; infection; autoimmune disease; inflammation;
 KW quality assurance; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT i. .364
 FT /note= "extracellular region"

FT Peptide 1. .20
 FT /note= "signal peptide"
 FT Domain 365. .385
 FT /note= "transmembrane domain"
 FT Domain 386. .432
 FT /note= "cytoplasmic domain"
 XX
 XX WO200008057-A2.
 XX
 XX 17-FEB-2000.
 XX
 XX 05-AUG-1999; 99WO-US017906.
 XX
 XX 07-AUG-1998; 98US-0095663P.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Baum PE;
 XX
 XX WPI; 2000-205674/18.
 XX
 XX N-PSDB; AA261416.
 XX
 XX Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
 FT costimulatory molecules for therapeutics against infections, autoimmune
 FT diseases and inflammation.
 XX
 XX Claim 8; Page 40-41; 57pp; English.
 XX
 CC The present sequence represents the long extracellular form of human B7-1
 CC (CD80). B7-1 is a T-cell costimulatory molecule that is found on the
 CC surface of antigen presenting cells (APCs). CD28 and CTLA4 are its T cell
 CC surface receptors. B7-1 interacts with CD28 to signal cytokine and memory
 CC production, cell proliferation, and the generation of effector and memory
 CC T cells. Disorders mediated by interaction of B7-1 and its binding
 CC partner, such as infections, autoimmune diseases and inflammation, are
 CC treated by administering B7L-1 to the diseased mammal. B7L-1
 CC polypeptides are useful to separate cells expressing a protein to which
 CC it binds and to measure the biological activity of LDCAM polypeptides.
 CC They can also be used as reagents for conducting quality assurance
 CC studies e.g., to monitor shelf life and stability of proteins to which it
 CC binds, and as carriers for delivering agents attached to cells bearing
 CC its counter structure, LDCAM or other cell receptors. They are also
 CC useful as a research tool for studying T-cell signalling and
 CC proliferation. They are employed in in vitro assays for detecting
 CC interactions of LDCAM with T-cell receptors. Diagnostic and therapeutic
 CC agents, such as drugs, toxins, radionuclides, chromophores, and enzymes
 CC which catalyse a colorimetric or fluorometric reaction, may be attached
 CC to a B7L-1 polypeptide, e.g. nitrogen mustards are attached to the B7L-1
 CC and used to treat various forms of cancer
 XX
 XX Sequence 432 AA;

Query Match 100.0%; Score 2264; DB 3; Length 432;
 Best Local Similarity 100.0%; Pred. No. 9.9e-164;
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQDLELGTAPLDEAISTVWSSPDML 60
 QY 61 ASQDSQPWTSDETVAAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIOIV 120
 Db 61 ASQDSQPWTSDETVAAGTVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIOIV 120
 QY 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSLREKD 180
 Db 121 TSTPHELISISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSLREKD 180
 QY 181 TATLNCQSSGSKPAARLTWRKGDDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 Db 181 TATLNCQSSGSKPAARLTWRKGDDELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGAS 240
 QY 241 IVCSNVHESLKGADRSQRIEVLVYPTAMRDPDPHPRGQKLLHCEGRGNVPVQOYL 300


```
RA Sudhof T.C.;
RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly.";
RL Science 0:0-0(2002).
DR EMBL; AF539424; AAN01614.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; F:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR KMW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match 31.8%; Score 719.5; DB 11; Length 445;
Best Local Similarity 36.2%; Pred. No. 4.8e-51;
Matches 166; Conservative 75; Mismatches 140; Indels 77; Gaps 10;

QY 9 LLLLLLFFACWAPGAGNLSQDGYWQEQDLELGLTAPLDEALISSTVWSPPDMLASQDSQPW 68
DB 31 LLLLLLSAAALIPG-----DG-----QNL-----F 51

QY 69 TSDETIVAGGVVLKQVKHEDSSQWSNAQOTLYFGKRALRDNRIQVLTSTPHEL 128
DB 112 VSLTNVSISSDEGRFCQYTDPPQESYTIIVLPPRLMIDIQDIAVEGEEIEVNCTA 171

QY 129 ISISNVALADRGYTCSTFTMPVKTAKSLVTLGIPQKPIITGYKSLREKDTATLNCQS 188
DB 112 VSLTNVSISSDEGRFCQYTDPPQESYTIIVLPPRLMIDIQDIAVEGEEIEVNCTA 171

QY 189 SGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKFTVSSSVTFQVTRDDGASIVCSVNHE 248
DB 172 MASKPATTTIRWFKGNKELKKG-SEVEEWS--MYTVTSQMLKVHKEDDGVFVICQVEHP 228

QY 249 SLKGADSTSORIEVLYPTTAMIRPDPP---HPREGQKLLHCEGRGNPVPQQYLWEK-E 304
DB 229 AVTG-NLQTORILEYQYKPVQVHIQMTYPLQGLTREGDAFELTCEAIGKQPQVMTVVRVD 287

QY 305 GSVPLKMTQBSALIFPPLNKSDGTGCTATSNMGSYKAVYTLNNDPS---PVPSSSS 361
DB 288 DEMQHAVLSCGNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLVYDPTTIPPTIT 347

QY 362 TY-----HAIIGGIVAFIVFLLLIMLIFLGHYLIIRHG 394
DB 348 TTTTNTTTSILTIITDSRAGEGTIGAVDHAIVGGVAVVVFAMLCLLIILGRYFARHG 407

QY 395 TYLTAEKGSDDADPADTAIINAEQGSGGDDKKEYFI 432
DB 408 TYFTAEKAGDADAADTAIINAEQGQNNSEKKEYFI 445
```

Search completed: May 27, 2004, 09:34:57

Job time : 36.4266 secs

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK001560; BAA91756.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurexin-like.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Hypothetical protein; Immunoglobulin domain.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 163 AA; 17860 MW; FB746375A05B0006 CRC64;

Query Match 38.5%; Score 872; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 2.7e-64;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 MIRPDPPHREGQKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSG 329
Db 1 MIRPDPPHREGQKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSG 60

QY 330 TYGCTATSNMGSKAYTYTNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 389
Db 61 TYGCTATSNMGSKAYTYTNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 120

QY 390 IRHKGTYLTHEAGSDADPADTAIINAEQGSGGDDKKEYFI 432
Db 121 IRHKGTYLTHEAGSDADPADTAIINAEQGSGGDDKKEYFI 163

RESULT 13
Q8K1H8 PRELIMINARY; PRT; 163 AA.
AC Q8K1H8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to hypothetical protein FLJ10698.
GN NECL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAUBERG R.;
RC TISSUE=Retina;
RA Strauberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029659; AAR29659.1; -
DR MGD; MGI:2137858; Nec11.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGC; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Hypothetical protein; Immunoglobulin domain.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 163 AA; 17773 MW; IDBA707A03B71BBA CRC64;

Query Match 36.7%; Score 831; DB 11; Length 163;
Best Local Similarity 95.1%; Pred. No. 6.7e-61;
Matches 155; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 270 MIRPDPPHREGQKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSG 329
Db 1 MIRPDPPHREGQKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSG 60

QY 330 TYGCTATSNMGSKAYTYTNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 389
Db 61 TYGCTATSNMGSKAYTYTNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 120

Db 61 TYGCTATSNMGSKAYTYTNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYL 120
QY 390 IRHKGTYLTHEAGSDADPADTAIINAEQGSGGDDKKEYFI 432
Db 121 IRHKGTYLTHEAGSDADPADTAIINAEQGSGGDDKKEYFI 163

RESULT 14
Q8BSQ8 PRELIMINARY; PRT; 152 AA.
AC Q8BSQ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like 1 (Fragment).
GN NECL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK030782; BAC27137.1; -
DR MGD; MGI:2137858; Nec11.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 152 AA; 16458 MW; E41F6BAAD6A413A7 CRC64;

Query Match 34.3%; Score 777; DB 11; Length 152;
Best Local Similarity 96.1%; Pred. No. 1.8e-56;
Matches 146; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 281 GOKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG 340
Db 1 GOKLLHCEGRGNVPVQQYLWEKGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMG 60

QY 341 SYKAYTYTNVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYLIRHKGTYLTHE 400
Db 61 SYTAYFTLVNDPSPVSSSTYHAIIGGIVAFIVFLMLIFLGHYLIRHKGTYLTHE 120

QY 401 AKGSDADPADTAIINAEQGSGGDDKKEYFI 432
Db 121 AKGSDADPADTAIINAEQGSGGDDKKEYFI 152

RESULT 15
Q8K3T6 PRELIMINARY; PRT; 445 AA.
AC Q8K3T6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,

```
QY 359 SSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGYTLTHEAKGSDPADADTAIINAE 418
DB 322 QNGPDHALIGGIVAVVVFVLCISFLIGRYLARHKGTYLTNEAKGAEDAPADTAIINAE 381
QY 419 GQSGGDDKKKEYFI 432
DB 382 GSQVNAEKKKEYFI 395

RESULT 10
Q8N3J6 PRELIMINARY; PRT; 435 AA.
AC Q8N3J6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKF2P761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amysdaia;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDJ databases.
EMBL; AL834270; CAD36945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein, Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F3D446 CRC64;

Query Match 44.9%; Score 1017.5; DB 4; Length 435;
Best Local Similarity 48.6%; Pred. No. 9.6e-76;
Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;

QY 62 SQDSQWTSDETVAGTIVLKCQVXKDESSLOWNSPAQOTLYFGEKALRDNRIQVLT 121
DB 22 SQGQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQNSNPAQOTLYFDKKALRDNRIELVR 81
QY 122 STPHLSISISNVALADEGYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKDT 181
DB 82 ASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSPVMEGL 141
QY 182 ATLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKTFVSSVTTQVTRDDGASI 241
DB 142 MQLTCTSGSKPAADIRWFKNDEIKDVYKLBEDANRKTFTVSSSLDFRVDSDGVAV 201
QY 242 VCSVNHEISLKGADRSQRIEVLVTPMTAPRPPHREGQKLLHCEGRGNVPVQYIWM 301
DB 202 ICRVDHESLNATPQAMQVLEIHYTPSVKLIPTFPQEGPPLITCESKGPLPEPVLW 261
QY 302 EKEGVS---PPLKMTQESALIFFLNKSDSGTCTATSNMGSYKAYTILNVND----- 352
DB 262 TKDGGELPDPDRMVSVGRELNILFLNKTNGTYRCEATNTIGQSAEYVLIIVHVDVENTLL 321
QY 353 PPSV-----PSSSSTY-----HAIIGGIVAFIVFLL 378
DB 322 PTTIIPSLTATVTTVAITTSPTTSATSSIRDPNALAGQPGDHALIGGIVAVVVFVT 381
QY 379 LIMLIFLGHYLIRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKKEYFI 432
DB 382 LCSIFLLGRYLARHKGTYLTNEAKGAEDAPADTAIINAEQSQVNAEKKKEYFI 435
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RESULT 11
Q8I2P8

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ID Q8I2P8 PRELIMINARY; PRT; 437 AA.
AC Q8I2P8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nectin-like protein 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gingrich J.R., D'Angelo A., Chang G.M., Greenberg N.M.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DDJ databases.
EMBL; AF538973; AAN16368.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 437 AA; 47593 MW; D23DB347F5E5F023 CRC64;

Query Match 44.8%; Score 1014.5; DB 4; Length 437;
Best Local Similarity 48.6%; Pred. No. 1.7e-75;
Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;

QY 62 SQDSQWTSDETVAGTIVLKCQVXKDESSLOWNSPAQOTLYFGEKALRDNRIQVLT 121
DB 24 SQGQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQNSNPAQOTLYFDKKALRDNRIELVR 83
QY 122 STPHLSISISNVALADEGYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKDT 181
DB 84 ASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSPVMEGL 143
QY 182 ATLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKTFVSSVTTQVTRDDGASI 241
DB 144 MQLTCTSGSKPAADIRWFKNDEIKDVYKLBEDANRKTFTVSSSLDFRVDSDGVAV 203
QY 242 VCSVNHEISLKGADRSQRIEVLVTPMTAPRPPHREGQKLLHCEGRGNVPVQYIWM 301
DB 204 ICRVDHESLNATPQAMQVLEIHYTPSVKLIPTFPQEGPPLITCESKGPLPEPVLW 263
QY 302 EKEGVS---PPLKMTQESALIFFLNKSDSGTCTATSNMGSYKAYTILNVND----- 352
DB 264 TKDGGELPDPDRMVSVGRELNILFLNKTNGTYRCEATNTIGQSAEYVLIIVHVDVENTLL 323
QY 353 PPSV-----PSSSSTY-----HAIIGGIVAFIVFLL 378
DB 324 PTTIIPSLTATVTTVAITTSPTTSATSSIRDPNALAGQPGDHALIGGIVAVVVFVT 383
QY 379 LIMLIFLGHYLIRHKGYTLTHEAKGSDPADADTAIINAEQSGGDDKKKEYFI 432
DB 384 LCSIFLLGRYLARHKGTYLTNEAKGAEDAPADTAIINAEQSQVNAEKKKEYFI 437

RESULT 12
Q8NVJ5 PRELIMINARY; PRT; 163 AA.
AC Q8NVJ5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ10698.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
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Db 204 SDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKIIPTSTPPQBGQALTLTCSKGP 263
Qy 295 VPOQYLWEKGSV---PPLKMTQESALIPFLNKS DSGTVCATSNMGSYKAYTYTLNW 351
Db 264 LPEPLVNTKGAELPDPDRMVSGRELNLFNKTNGTYRCEATNTIGQSSAYVLIH 323
Qy 352 DPSFVSSSTVHAITGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDAPDAD 411
Db 324 DPNSLAGQNDHALIGGIVAVVVFVTLCSIFILGRLARHKGTYLTHEAKGSDDDAPDAD 383
Qy 412 TAIINAEQSGSGDDKKEYFI 432
Db 384 TAIINAEQSGVNAEKKKEYFI 404

RESULT 8
ID Q8BZP4 PRELIMINARY; PRT; 395 AA.
AC Q8BZP4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dienecephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK033973; BAC28533.1; -
DR MGD; MGI:2442722; A830029E02Rik.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003598; IG c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 395 AA; 43516 MW; EB70FB5363D872F3 CRC64;

Query Match 46.0%; Score 1042.5; DB 11; Length 395;
Best Local Similarity 52.9%; Pred. No. 7.le-78;
Matches 198; Conservative 68; Mismatches 105; Indels 3; Gaps 1;

Qy 62 SQDSQWTSDETAVAGTVVLCQVKKHEDSSLOWSNPAQOTLYFGKRALRNRIOLVT 121
Db 22 SQQFPLTQNVVVEGTAITLCRVQDNDNTSLQSNPAQOTLYFDDKKALRNRIELVR 81
Qy 122 STPELSISINVALADEGETCSIFTMPVRTAKSLVTLVIGIPKPIITGYKSSLRKDT 181
Db 82 ASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYITLVIGPEKPGISGFSSPMEGDL 141
Qy 182 ATLNCSGSGKPAARLTWRKQDQELHGEPTRIQEDPNKGTFTVSSSVTFVTRDDGASI 241
Db 82 ASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYITLVIGPEKPGISGFSSPMEGDL 141
Qy 182 ATLNCSGSGKPAARLTWRKQDQELHGEPTRIQEDPNKGTFTVSSSVTFVTRDDGASI 241
Db 142 MQLTCKTSGSKPAADIRFNKNDKEIKDVLYKEDANRKTFTVSTLDFRVDSDGAV 201
Qy 242 VCSVNHSLKGDARSTSRILEVLYTPTAMIRPDPPHREGOKLLHCEGRGNVPQOYLW 301
Db 202 ICRVDHESLNATPQVAMQVLEIHYTPSVKIIPTSTPPQBGQALTLTCSKGPPLPEVLW 261
Qy 302 EKEGSV---PPLKMTQESALIPFLNKS DSGTVCATSNMGSYKAYTYTLNWDPSPVPS 358
Db 302 EKEGSV---PPLKMTQESALIPFLNKS DSGTVCATSNMGSYKAYTYTLNWDPSPVPS 358
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Db 262 TKGAEPLPDPDRMVSGRELNLFNKTNGTYRCEATNTIGQSSAYVLIHDPNSLAG 321
Qy 359 SSVTHAITGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDDAPDADTAIINAE 418
Db 322 QNGPHALIGGIVAVVVFVTLCSIFILGRLARHKGTYLTHEAKGSDDDAPDADTAIINAE 381
Qy 419 GQSGGDDKKEYFI 432
Db 382 GQVNAEKKKEYFI 395

RESULT 9
ID Q8BXJ7 PRELIMINARY; PRT; 395 AA.
AC Q8BXJ7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK046800; BAC32876.1; -
DR MGD; MGI:2442722; A830029E02Rik.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; IG; 3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 395 AA; 43517 MW; E57E1BBD6D3672F9 CRC64;

Query Match 46.0%; Score 1042.5; DB 11; Length 395;
Best Local Similarity 52.9%; Pred. No. 7.le-78;
Matches 198; Conservative 68; Mismatches 105; Indels 3; Gaps 1;

Qy 62 SQDSQWTSDETAVAGTVVLCQVKKHEDSSLOWSNPAQOTLYFGKRALRNRIOLVT 121
Db 22 SQQFPLTQNVVVEGTAITLCRVQDNDNTSLQSNPAQOTLYFDDKKALRNRIELVR 81
Qy 122 STPELSISINVALADEGETCSIFTMPVRTAKSLVTLVIGIPKPIITGYKSSLRKDT 181
Db 82 ASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYITLVIGPEKPGISGFSSPMEGDL 141
Qy 182 ATLNCSGSGKPAARLTWRKQDQELHGEPTRIQEDPNKGTFTVSSSVTFVTRDDGASI 241
Db 142 MQLTCKTSGSKPAADIRFNKNDKEIKDVLYKEDANRKTFTVSTLDFRVDSDGAV 201
Qy 242 VCSVNHSLKGDARSTSRILEVLYTPTAMIRPDPPHREGOKLLHCEGRGNVPQOYLW 301
Db 202 ICRVDHESLNATPQVAMQVLEIHYTPSVKIIPTSTPPQBGQALTLTCSKGPPLPEVLW 261
Qy 302 EKEGSV---PPLKMTQESALIPFLNKS DSGTVCATSNMGSYKAYTYTLNWDPSPVPS 358
Db 262 TKGAEPLPDPDRMVSGRELNLFNKTNGTYRCEATNTIGQSSAYVLIHDPNSLAG 321
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QY 1 MGAPAAALLLLLLLACCWAPGANLSQDQWQOQLELGTAPLDEALISSTVWSPDML 60
Db 1 MGAPAAALLLLLLLACCWAPGANLSQD-----29
QY 61 ASOSQSWTSDETVVAGTGVVVKQVXDHDSSLOWSNPAQOTLYFGKALRDNRIQV 120
Db 30 --DSQSWTSDETVVAGTGVVVKQVXDHDSSLOWSNPAQOTLYFGKALRDNRIQV 86
QY 121 TSPHLSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSPHLSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTVSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDND-----185
QY 241 IVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHREGOKLLHCEGRGNPVPQOYL 300
Db 186 -----TPTAMIRDPDPHREGOKLLHCEGRGNPVPQOYL 220
QY 301 WEKEGSVPPLKMTQ 314
Db 221 WEKEGSVPPLKMTQ 234
RESULT 6
ID QBYP1 PRELIMINARY; PRT; 404 AA.
AC QBYP1,
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK038842; BAC30148.1; -
DR MGD; MGI:2442722; A830029E02Rik.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 404 AA; 44387 MW; E9C84191AA687473 CRC64;

Query Match 46.1%; Score 1043.5; DB 11; Length 404;
Best Local Similarity 52.2%; Pred. No. 6.1e-78;
Matches 199; Conservative 69; Mismatches 110; Indels 3; Gaps 1;

QY 55 SSPDMLASQSQPWTSDTVVAGTGVVVKQVXDHDSSLOWSNPAQOTLYFGKALRDNRIQV 114
Db 24 SKSVKVGSGQGFPLTONVTVVEGGTALTTCRVQDNDNTSLQSNPAQOTLYFDDKKALRD 83
QY 115 NRILQVTSFHELSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 174
Db 84 NRILVRSWHELSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 143
QY 175 SLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTVSSVTFQVTR 234
Db 84 NRILVRSWHELSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 143
QY 175 SLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTVSSVTFQVTR 234
Db 144 PVMEGLMLQLTCTSGSKPAADIRFWFKNDKEIKDVVKYKKEEDANRKTFTVSSITLDFRVD 203
QY 235 EDDGASIVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHREGOKLLHCEGRGNP 294
Db 144 PVMEGLMLQLTCTSGSKPAADIRFWFKNDKEIKDVVKYKKEEDANRKTFTVSSITLDFRVD 203

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QY 235 EDDGASIVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHREGOKLLHCEGRGNP 294
Db 204 SDGVAIVICRVHESLNATPQVAMQVLEIHYTPSVKLIIFSTFPQEQALTLTCSKGRP 263
QY 295 VPQYLWEKEGSV---PPLKMTQESALIFPFLNKSDSGTCTATSNMGSYKAYITLVN 351
Db 264 LPEPVLTKDGAELPDPDRMVVSGRELNFLENKTDNGTYRCCKATNTIGQSSAEYVLIVH 323
QY 352 DSPVSSSTVHAITGGIVAFIVFLLLMFLHGLYLRHKGYTLTHEAKGSDDDAPDAD 411
Db 324 DPNSLAQGNPDPHALTGGIVAVVVFVTLCSIFLLGRTYLRHKGYTLTHEAKGSDAPDAD 383
QY 412 TAINAEGSGSGDDKKEYFI 432
Db 384 TAINAEGSQVNAEKKKEYFI 404
RESULT 7
ID QBLO9 PRELIMINARY; PRT; 404 AA.
AC QBLO9,
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK043760; BAC31646.1; -
DR MGD; MGI:2442722; A830029E02Rik.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR PRINTS; PR01474; VCAML.
DR SMART; SM00409; IGC2; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 404 AA; 44388 MW; 091E493B82CAFE5B CRC64;

Query Match 46.1%; Score 1043.5; DB 11; Length 404;
Best Local Similarity 52.2%; Pred. No. 6.1e-78;
Matches 199; Conservative 69; Mismatches 110; Indels 3; Gaps 1;

QY 55 SSPDMLASQSQPWTSDTVVAGTGVVVKQVXDHDSSLOWSNPAQOTLYFGKALRDNRIQV 114
Db 24 SKSVKVGSGQGFPLTONVTVVEGGTALTTCRVQDNDNTSLQSNPAQOTLYFDDKKALRD 83
QY 115 NRILQVTSFHELSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 174
Db 84 NRILVRSWHELSISISNVALADEGYTCISFTMPVRTAKSLVTVLGIPOKPIITGYKS 143
QY 175 SLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTVSSVTFQVTR 234
Db 144 PVMEGLMLQLTCTSGSKPAADIRFWFKNDKEIKDVVKYKKEEDANRKTFTVSSITLDFRVD 203
QY 235 EDDGASIVCSVNHESLKGDARSTSORIEVLYTPTAMIRDPDPHREGOKLLHCEGRGNP 294
Db 144 PVMEGLMLQLTCTSGSKPAADIRFWFKNDKEIKDVVKYKKEEDANRKTFTVSSITLDFRVD 203

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60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AF195662; AAG3584.1; -
DR EMBL; AY059393; AAL29691.1; -
DR EMBL; AK038917; BAC30168.1; -
DR EMBL; AK053077; BAC35258.1; -
DR MGD; MGI:2137858; Nccl1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 396 AA; 42964 MW; C1ADF8B57D141F3A CRC64;

Query Match 85.8%; Score 1943; DB 11; Length 396;
Best Local Similarity 87.3%; Pred. No. 1.8e-152;
Matches 377; Conservative 11; Mismatches 8; Indels 36; Gaps 2;

QY 1 MGAPASLLLLLLFACWAPGANLSQDGYWQEQDLEGLTAPLDEAISTVWSSPDL 60
DB 1 MGAPSA--LPLLLLLACSWAPGANLSQD----- 27

QY 61 ASQDSQPWTSDETVVAGGTIVLKCVKQKHEDSSLOWSNPAQOTLYFGKRALRDNRILQ 120
DB 28 ---DSQPWTSDETVVAGGTIVLKCVKQKHEDSSLOWSNPAQOTLYFGKRALRDNRILQ 84

QY 121 TSTPHELISISINVALADEGEYTCISFTMPVTRTAKSLVTLVGIPOKPIITGYKSLREKD 180
DB 85 SSTPHELISISINVALADEGEYTCISFTMPVTRTAKSLVTLVGIPOKPIITGYKSLREKE 144

QY 181 TATLNCQSGSGSPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGAS 240
DB 145 TATLNCQSGSGSPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGAS 204

QY 241 IVCSNVHESLKGADRTSQRIEVLVYPTAMIRDPHPHREGOKLLHCEGRGNVPVQQYL 300
DB 205 IVCSNVHESLKGADRTSQRIEVLVYPTAMIRDPHPHREGOKLLHCEGRGNVPVQQYL 264

QY 301 WEKESVPLKMTQESALIFPFLNKSQDGTCTATSNMGSKYKAYITLVNNDPSPVPSS 360
DB 265 WEKESVPLKMTQESALIFPFLNKSQDGTCTATSNMGSKYKAYITLVNNDPSPVPSS 324

QY 361 STYHAIIGGIVAFIVFLLLIMLIFLGHVLIHKGTYLTAEAGSDDAPDADTAIINAE 420
DB 325 STYHAIIGGIVAFIVFLLLIMLIFLGHVLIHKGTYLTAEAGSDDAPDADTAIINAE 384

QY 421 QSGGDDKKEYFI 432
DB 385 QSGGDDKKEYFI 396

RESULT 4
Q7ZXX1 PRELIMINARY; PRT; 394 AA.
AC Q7ZXX1;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to nectin-like 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044084; AAH44084.1; -

60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AF195662; AAG3584.1; -
DR EMBL; AY059393; AAL29691.1; -
DR EMBL; AK038917; BAC30168.1; -
DR EMBL; AK053077; BAC35258.1; -
DR MGD; MGI:2137858; Nccl1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 396 AA; 42964 MW; C1ADF8B57D141F3A CRC64;

Query Match 85.8%; Score 1262.5; DB 13; Length 394;
Best Local Similarity 64.8%; Pred. No. 4.2e-96;
Matches 239; Conservative 51; Mismatches 78; Indels 1; Gaps 1;

QY 65 SQPWTSDTVVAGGTIVLKCVKQKHEDSSLOWSNPAQOTLYFGKRALRDNRILQVHTSP 124
DB 26 SQPVTADVIVTGGTALIKCTVQEHLESSLOWSNPAQOTLYFGKRALRDNRILQVHTSP 85

QY 125 HELSISINVALADEGEYTCISFTMPVTRTAKSLVTLVGIPOKPIITGYKSLREKDTATL 184
DB 86 NELTISINVVLSDEGEYTCISFTMPVTRTAKAVVTVLGVGPQVSGFSAFKENDKAKL 145

QY 185 NCQSGSGSPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGASIVCS 244
DB 146 RCTTSGSGSPAANIKWYKGPPELEGAKTSLVDGNGKTFVKSFIETVTKDDGAEITCA 205

QY 245 VNHESLKGADRTSQRIEVLVYPTAMIRDPHPHREGOKLLHCEGRGNVPVQQYLWEKE 304
DB 206 VGHESLHDSAKSSSHKIQVQYKTKAKIESRPSMPREGDKLRLQCDAYGNVPDNYWVERE 265

QY 305 -GSVPLKMTQESALIFPFLNKSQDGTCTATSNMGSKYKAYITLVNNDPSPVPSSSTY 363
DB 266 NGEVELLANIEGNSLVFENLNKTDGTYTCKASNTLGTFTYHKLDVNDPSPIPSTSID 325

QY 364 HAITGGIVAFIVFLLLIMLIFLGHVLIHKGTYLTAEAGSDDAPDADTAIINAE 423
DB 326 HAVIGGVAVATFLIFCLLIVLGRYLIHKGTYLTAEAGSDDAPDADTAIINAE 385

QY 424 GDDKKEYFI 432
DB 386 SDDKKEYFI 394

RESULT 5
Q8IZQ9 PRELIMINARY; PRT; 234 AA.
AC Q8IZQ9;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Dendritic cell nectin-like protein 1 short isoform (Fragment).
GN NECL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keryanov S.A., Gardner K.L.;
RT "Alternatively splicing forms of the human nectin V gene.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF529206; AAN75603.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 25655 MW; 8DA496486BE1CCB CRC64;

Query Match 51.9%; Score 1176; DB 4; Length 234;
Best Local Similarity 74.2%; Pred. No. 2.9e-89;
Matches 233; Conservative 0; Mismatches 1; Indels 80; Gaps 2;

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Db 1 MGAPASLLLLLLLACCCWAPGANLSQDGYWQDLELGTALPLDEAISSTVWSSPDML 60
QY 61 ASQDSQWTSDETVVAGTGVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 120
Db 61 ASQDSQWTSDETVVAGTGVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 120
QY 121 TSTPHELSISINVALADEGEYTCISFTMPVTRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 121 TSTPHELSISINVALADEGEYTCISFTMPVTRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
Db 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
QY 241 IVCSVNHESLKGDARSTSORIEVLYPTAMIRPPPHREGOKLLHCEGRGNVPVPOYL 300
Db 241 IVCSVNHESLKGDARSTSORIEVLYPTAMIRPPPHREGOKLLHCEGRGNVPVPOYL 300
QY 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDPSPVPSSS 360
Db 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDPSPVPSSS 360
QY 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLIHRHKGTYLTHEAKGSDPADADTAIINAE 420
Db 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLIHRHKGTYLTHEAKGSDPADADTAIINAE 420
QY 421 QSGGDDKKEYFI 432
Db 421 QSGGDDKKEYFI 432

RESULT 2
Q8N126 PRELIMINARY; PRT; 398 AA.
ID Q8N126;
AC Q8N126;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Brain immunoglobulin receptor precursor (Nectin-like protein 1)
DE (TSLC1-like 1).
GN TSLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Brain;
RC TISSUE=Brain;
RA Cunningham S.A., Tran T.M., Arrate M.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Fukuhara H., Murakami Y.;
RT "Isolation of the TSLC1 and TSLC2 genes, members of the tumor
RT suppressor TSLC1 gene family encoding transmembrane proteins.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY046418; AAL02143.1; -
DR EMBL; BC033819; AAB33819.1; -
DR EMBL; AF363367; AAM60749.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR007398; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
```

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KW Immunoglobulin domain; Receptor; Signal.
FT SIGNAL 1 24 POTENTIAL.
SQ SEQUENCE 398 AA; 43300 MW; 601B2FB5D512DB6C CRC64;

Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 4.4e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPASLLLLLLLACCCWAPGANLSQDGYWQDLELGTALPLDEAISSTVWSSPDML 60
Db 1 MGAPASLLLLLLLACCCWAPGANLSQD----- 29
QY 61 ASQDSQWTSDETVVAGTGVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 120
Db 30 --DSQDQWTSDETVVAGTGVVLCQVKDHDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 86
QY 121 TSTPHELSISINVALADEGEYTCISFTMPVTRTAKSLVTVLGIPOKPIITGYKSSLRKD 180
Db 87 TSTPHELSISINVALADEGEYTCISFTMPVTRTAKSLVTVLGIPOKPIITGYKSSLRKD 146
QY 181 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
QY 241 IVCSVNHESLKGDARSTSORIEVLYPTAMIRPPPHREGOKLLHCEGRGNVPVPOYL 300
Db 207 IVCSVNHESLKGDARSTSORIEVLYPTAMIRPPPHREGOKLLHCEGRGNVPVPOYL 266
QY 301 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDPSPVPSSS 360
Db 267 WEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDPSPVPSSS 326
QY 361 STYHAIIGGIVAFIVFLLLMILIFLGHYLIHRHKGTYLTHEAKGSDPADADTAIINAE 420
Db 327 STYHAIIGGIVAFIVFLLLMILIFLGHYLIHRHKGTYLTHEAKGSDPADADTAIINAE 386
QY 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 3
Q99N28 PRELIMINARY; PRT; 396 AA.
ID Q99N28;
AC Q99N28;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein) (Nectin-like 1).
GN NECL1 OR TSL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RT "Cloning and expression analysis of novel mouse cDNA encoding a
RT membrane protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Fukami T., Maruyama T., Murakami Y.;
RT "Identification of a murine ortholog of the TSLC1-like gene 1.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 35.4266 Seconds
(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187B-8
Perfect score: 2264

Sequence: 1 MGAPASLRLLLLLFACCA.....AIIAAGGQSGGDKKEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2264	100.0	432	4 Q9UJ1	Q9UJ1 homo sapien
2	2059	90.9	398	4 Q8N126	Q8N126 homo sapien
3	1943	85.8	396	11 Q9N28	Q9N28 mus musculus
4	1262.5	55.8	394	13 Q7XX1	Q7XX1 xenopus lae
5	1176	51.9	234	4 Q81Q9	Q81Q9 homo sapien
6	1043.5	46.1	404	11 Q8BYF1	Q8BYF1 mus musculus
7	1043.5	46.1	404	11 Q8BLQ9	Q8BLQ9 mus musculus
8	1042.5	46.0	395	11 Q8BZP4	Q8BZP4 mus musculus
9	1042.5	46.0	395	11 Q8BXJ7	Q8BXJ7 mus musculus
10	1017.5	44.9	435	4 Q8N3J6	Q8N3J6 homo sapien
11	1014.5	44.8	437	4 Q812P8	Q812P8 homo sapien
12	872	38.5	163	4 Q9NVJ5	Q9NVJ5 homo sapien
13	831	36.7	163	11 Q8X1H8	Q8X1H8 mus musculus
14	777	34.3	152	11 Q8BSQ8	Q8BSQ8 mus musculus
15	719.5	31.8	445	11 Q8K3T6	Q8K3T6 mus musculus
16	719.5	31.8	445	11 Q8R4L1	Q8R4L1 mus musculus

17	719	31.8	442	4 Q9BY67	Q9BY67 homo sapien
18	710.5	31.4	417	11 Q7TNL1	Q7TNL1 mus musculus
19	709	31.3	456	11 Q8R5M6	Q8R5M6 mus musculus
20	707.5	31.2	443	4 Q8N2F4	Q8N2F4 homo sapien
21	594	26.2	388	4 Q8NFZ8	Q8NFZ8 homo sapien
22	583	25.8	388	11 Q8R464	Q8R464 mus musculus
23	576.5	25.5	381	4 Q9Y4A4	Q9Y4A4 homo sapien
24	514	22.7	295	11 Q9QYL6	Q9QYL6 mus musculus
25	510	22.5	295	11 Q9Z2H8	Q9Z2H8 mus musculus
26	508.5	22.5	306	11 Q9QYL4	Q9QYL4 mus musculus
27	503.5	22.2	278	11 Q9QYL3	Q9QYL3 mus musculus
28	499	22.0	289	11 Q9QYL5	Q9QYL5 mus musculus
29	457	20.2	333	4 Q8GWB8	Q8GWB8 homo sapien
30	454.5	20.1	336	11 Q9D6E7	Q9D6E7 mus musculus
31	454.5	20.1	336	11 Q8OVG4	Q8OVG4 mus musculus
32	328.5	14.5	403	6 Q8HY15	Q8HY15 lemur catta
33	295	13.0	412	6 Q8HY14	Q8HY14 oryctolagus
34	273.5	12.1	401	6 Q88835	Q88835 cercopithec
35	272	12.0	778	4 Q81ZU9	Q81ZU9 homo sapien
36	272	12.0	779	4 Q96JG0	Q96JG0 homo sapien
37	271	12.0	612	11 Q8BGQ5	Q8BGQ5 mus musculus
38	271	12.0	766	11 Q81OH3	Q81OH3 mus musculus
39	271	12.0	778	11 Q8BR86	Q8BR86 mus musculus
40	264	11.7	417	4 Q96B5J1	Q96B5J1 homo sapien
41	264	11.7	439	13 Q57349	Q57349 gallus gall
42	256	11.3	530	11 Q80XJ5	Q80XJ5 mus musculus
43	255	11.3	412	11 Q63611	Q63611 rattus norv
44	255	11.3	412	11 Q9R1E1	Q9R1E1 rattus norv
45	254.5	11.2	467	11 Q91VT9	Q91VT9 mus musculus

ALIGNMENTS

RESULT 1
Q9UJ1 PRELIMINARY; PRT; 432 AA.
ID Q9UJ1
AC Q9UJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BK134P22.1 (Novel protein similar to mouse IMMUNOSUPERFAMILY protein BL2) (NECTIN-like protein 1).
GN BK134P22.1 OR NECL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Yuan J., Qiang B.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035403; CAB56227.1; -.
DR EMBL; AF062733; AAD17540.2; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00294; IGC2; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 432 AA; 47020 MW; AC474EFEECC4C518C CRC64;

Query Match 100.0%; Score 2264; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 5, 2e-179;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPASLRLLLLLFACCA.....AIIAAGGQSGGDKKEYFI 432

DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; Ig; 5.
DR PRINTS; PR01472; ICAMVCAM1.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG_LIKE; 5.
KW Immunoglobulin domain; Glycoprotein; Cell adhesion; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 24 PROBABLE.
FT CHAIN 25 739 VASCULAR CELL ADHESION PROTEIN 1.
FT DOMAIN 25 698 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 699 720 POTENTIAL.
FT DOMAIN 721 739 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 111 IG-LIKE C2-TYPE 1.
FT DOMAIN 119 212 IG-LIKE C2-TYPE 2.
FT DOMAIN 223 309 IG-LIKE C2-TYPE 3.
FT DOMAIN 312 397 IG-LIKE C2-TYPE 4.
FT DOMAIN 408 506 IG-LIKE C2-TYPE 5.
FT DOMAIN 514 595 IG-LIKE C2-TYPE 6.
FT DOMAIN 601 682 IG-LIKE C2-TYPE 7.
FT DISULFID 47 95 BY SIMILARITY.
FT DISULFID 52 99 BY SIMILARITY.
FT DISULFID 137 195 BY SIMILARITY.
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 650 650 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 739 AA; 81246 MW; 5C608E5A1A1B100C CRC64;

Query Match 9.5%; Score 215; DB 1; Length 739;
Best Local Similarity 26.4%; Pred. No. 1.1e-07;
Matches 112; Conservative 45; Mismatches 176; Indels 92; Gaps 23;

QY 66 QPWTSD---ETVVA--GGTVVLKQVKDHEDSSLOWNPAAQQTLYFGEKRALRDNRIQL 119
Db 311 KPFTVDISPGSQVAAQVGSVLTCAAVGCDSPFSFWRQTDSPLN-GE---VRD---EG 363
QY 120 VTSTPHELISISNVALADEGYTCISFTMPVRTAKSL-VTVLIGIPQKPIITGYKSSLRE 178
Db 364 ATST----LTLSPGVGEDEHSVLCVTQCRRKLEKTIQVEVVSFFEDPEIE-ISGPLVH 417
QY 179 KDTATLNCQSSGSKPAARLTWRKGDQBLHGEPTR----TOEDPNGKTF-TVSSSVTFQVT 233
Db 418 GREVTVNTCTVNVYFPDHL- ----IELLKGETLLNKLFLREEIGTKSLKTSLEMTFTPT 473
QY 234 REDDGASIVGSVN-HESLKGADRSTSORIEVLT-----PTAMIRPDPPHREGQKLL 286
Db 474 AEDTGKALVCLAKLHSSQSEPKQKQSTQTLVNVVAPKEPTIWSVSPV-PEGSPVNL 532
QY 287 HCEGRGNVPQQYLWE---KEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSK 343
Db 533 TCSSDGFPTP-KILWSRQLKNGELQPL--SQNTLSFMATKMEDSGIYVCEGINEAGISK 589
QY 344 AYTLANVNDPS-----PVPSSSTYHAIIG---GIYAFIVELJ-----LIMLIF 384
Db 590 KVELIIQSSKDIQLTVFPKSVKEGDTVIIISCTGSPVEIWIILKKAKTGDWIKSV 649
QY 385 LGHYLIR-----HKGTY-----LTHEAKGSDDAPD-----ADTAI 414
Db 650 NGSYTIRKAQLQDAGVYECSEKTEVGSQRLSLTLDVYKKNKDYFSPPELLALYFASLV 709
QY 415 INAEQ 419
Db 710 IPAIG 714

Search completed: May 27, 2004, 09:35:45
Job time : 10.1752 secs

EMBL	M17303	AA059513.1	-	ALU_SEQ.
EMBL	M59262	AA062835.1	-	JOINED.
EMBL	M59255	AA062835.1	-	JOINED.
EMBL	M59257	AA062835.1	-	JOINED.
EMBL	M59258	AA062835.1	-	JOINED.
EMBL	M59259	AA062835.1	-	JOINED.
EMBL	M59260	AA062835.1	-	JOINED.
EMBL	M59261	AA062835.1	-	JOINED.
EMBL	M59709	-	-	NOT ANNOTATED CDS.
EMBL	M59710	-	-	NOT ANNOTATED CDS.
EMBL	M29540	AA051967.1	-	-
EMBL	X16455	CAA34474.1	-	-
EMBL	M15042	AA051963.1	-	-
EMBL	M16234	AA051972.1	-	-
PIR	A36319	A36319	-	-
PDB	1E07	04-JUL-00	-	-
Gene	Genew	HGNC:1817	-	CEACAM5.
MM	114890	-	-	-
GO	GO:0005887	C: integral to plasma membrane	-	TAS.
InterPro	IPR007110	IG-Like	-	-
Pfam	PF00047	ig	-	6.
PROSITE	PS00835	IG_LIKE	-	6.
Immunoglobulin domain	-	-	-	-
Glycoprotein	-	-	-	-
Lipoprotein	-	-	-	-
GPI-anchor	-	-	-	-
Membrane	-	-	-	-
Signal	-	-	-	-
Repeat	-	-	-	-
3D-structure	-	-	-	-
SIGNAL	1	34	-	-
CARCINOEMBRYONIC ANTIGEN-RELATED CELL	35	685	-	-
ADHESION MOLECULE 5	686	702	-	-
REMOVED IN MATURE FORM (POTENTIAL)	35	144	-	-
IG-LIKE 1.	146	237	-	-
IG-LIKE 2.	238	322	-	-
IG-LIKE 3.	324	415	-	-
IG-LIKE 4.	416	498	-	-
IG-LIKE 5.	502	593	-	-
IG-LIKE 6.	594	677	-	-
IG-LIKE 7.	685	685	-	-
GPI-anchor amidated alanine (Potential)	104	104	-	-
N-LINKED (GLCNAC. .)	115	115	-	-
N-LINKED (GLCNAC. .)	152	152	-	-
N-LINKED (GLCNAC. .)	182	182	-	-
N-LINKED (GLCNAC. .)	197	197	-	-
N-LINKED (GLCNAC. .)	204	204	-	-
N-LINKED (GLCNAC. .)	208	208	-	-
N-LINKED (GLCNAC. .)	246	246	-	-
N-LINKED (GLCNAC. .)	256	256	-	-
N-LINKED (GLCNAC. .)	274	274	-	-
N-LINKED (GLCNAC. .)	288	288	-	-
N-LINKED (GLCNAC. .)	292	292	-	-
N-LINKED (GLCNAC. .)	309	309	-	-
N-LINKED (GLCNAC. .)	330	330	-	-
N-LINKED (GLCNAC. .)	351	351	-	-
N-LINKED (GLCNAC. .)	360	360	-	-
N-LINKED (GLCNAC. .)	375	375	-	-
N-LINKED (GLCNAC. .)	432	432	-	-
N-LINKED (GLCNAC. .)	466	466	-	-
N-LINKED (GLCNAC. .)	480	480	-	-
N-LINKED (GLCNAC. .)	508	508	-	-
N-LINKED (GLCNAC. .)	529	529	-	-
N-LINKED (GLCNAC. .)	553	553	-	-
N-LINKED (GLCNAC. .)	560	560	-	-
N-LINKED (GLCNAC. .)	580	580	-	-
N-LINKED (GLCNAC. .)	612	612	-	-
N-LINKED (GLCNAC. .)	650	650	-	-
N-LINKED (GLCNAC. .)	665	665	-	-
N-LINKED (GLCNAC. .)	320	320	-	-
MISSING (IN REF. 4)	702	702	-	-
SEQUENCE	702	76795	MM	6299AE26CDDDB5C CRC64;
Score	216.5	DB 1	Length	702;
Local Similarity	27.7%			Pred. No. 8.1e-08;

DR HSSP; P19320; 1VCA.
DR InterPro; IPR003987; ICAM_VCAM-1.
DR InterPro; IPR007110; Ig-Like.

or send an email to license@isb-sib.ch).

```
CC CC -----
DR DR EMBL; U95030; AAC06342.1; -.
DR DR EMBL; L25274; AAA37528.1; -.
DR DR HSSP; Q13740; 1KJC.
DR DR MGD; MGI:1313266; Alcam.
DR DR GO; GO:0019997; C:extrinsic to plasma membrane; IDA.
DR DR GO; GO:0007165; P:signal transduction; IPT.
DR DR InterPro; IPR007110; Ig-like.
DR DR InterPro; IPR003599; Ig.
DR DR InterPro; IPR003006; Ig_MHC.
DR DR Pfam; PF00047; Ig; 4.
DR DR SMART; SM00409; IG; 3.
DR DR PROSITE; PS00835; IG LIKE; 4.
DR DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
FT FT Repeat; Signal.
FT FT SIGNAL 1 27 POTENTIAL.
FT FT CHAIN 28 583 CD166 ANTIGEN.
FT FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 528 549 POTENTIAL.
FT FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT FT DOMAIN 28 120 IG-LIKE V-TYPE 1.
FT FT DOMAIN 125 234 IG-LIKE V-TYPE 2.
FT FT DOMAIN 245 328 IG-LIKE C2-TYPE 1.
FT FT DOMAIN 333 409 IG-LIKE C2-TYPE 2.
FT FT DOMAIN 416 501 IG-LIKE C2-TYPE 3.
FT FT DISULFID 43 113 POTENTIAL.
FT FT DISULFID 157 220 POTENTIAL.
FT FT DISULFID 270 313 POTENTIAL.
FT FT DISULFID 354 392 POTENTIAL.
FT FT DISULFID 435 485 POTENTIAL.
FT FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CONFLICT 227 232 PSSGKT -> AAGIPA (IN REF. 2).
FT FT CONFLICT 454 454 S -> F (IN REF. 2).
SQ SQ SEQUENCE 583 AA; 65161 MW; 878486 CAS; 9489 CRC64;

Query Match 9.6%; Score 217.5; DB 1; Length 583;
Best Local Similarity 24.1%; Pred. No. 5.3e-08;
Matches 89; Conservative 49; Mismatches 143; Indels 89; Gaps 15;

QY 77 GGTVLKQVCKHEDSSLOWNSPAQOTLYRGEK-----ALRDNRIQLV----- 120
DB 36 GDTIVMPCRL-----DVPQNLMFGRKWKYKPDGSPVFIAPRSSTKKSQVDDV 83
QY 121 -----TSTPHELSISISVALADEGYTCISFIMP-VRTAKSLVTVLGIPOKPIITGYK 173
DB 84 PEYKDRLSLSENYTLISANAKISDEKGFVCMVLTEDNVFEAPLVKFKQSPKPIVKA 143
QY 174 SSIREKDTATL-NCQSGSGSPARLTW-RKGD--QELHGEP-----RIQEDPNKGTFTVSS 226
DB 144 PFLETDQLKLGDCISDSYDPDGNITRYRNGKVLQPVGEVAILFKKEIDPGTQLYTVTS 203
QY 227 SVTFQVTRDDGASIVCSNVHSLKGADRTS-ORIEVLYTPTAMIR-----POPPHPREG 281
DB 204 SLEKTRSDIQMPTCSVTYSGSGKTYSEQEIFDIYPTQVTVLPPKNAIKREG 263
QY 282 QKLHLHCEGRGNVPVQOYLWEKEGSPFLKMTQESALIFPFLANKSDSGTCTATS--NM 339
DB 264 DNITLQCLGNGNPPPEFMYFLPQ--PEGIRSSNTYTLTDVRENATGDKCSLIDKKNM 321
QY 340 GSKA-----YTLNVN-----DPSV-----PSSSS 361
DB 322 AASTITVHWYLDLSLNPGRVETKIGDTLPVSCITISASRNATVMMKDNIRLSSPSFSS 381
QY 362 TYHAIIIGIV 371
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DB 382 LHYQDAGNYV 391
:: | |
RESULT 14
CEAS_HUMAN
ID CEAS_HUMAN STANDARD; PRT; 702 AA.
AC P06731;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Carcinoembryonic antigen-related cell adhesion molecule 5 precursor
DE (Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66e
DE antigen).
GN CEACAM5 OR CEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90258861; PubMed=2342461;
RA Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,
RA Hassauer M., Shively J.E., von Kleist S., Zimmermann W.,
RT "Cloning of the complete gene for carcinoembryonic antigen: analysis
RT of its promoter indicates a region conveying cell type-specific
RT expression." RT
RL Mol. Cell. Biol. 10:2738-2748(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038876; PubMed=3670312;
RA Beauchemin N., Benchimol S., Cournoyer D., Fuks A., Stanners C.P.;
RT "Isolation and characterization of full-length functional cDNA clones
RT for human carcinoembryonic antigen." RT
RL Mol. Cell. Biol. 7:3221-3230(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89122014; PubMed=3220478;
RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
RT "Carcinoembryonic antigen family: characterization of cDNAs coding
RT for NCA and CEA and suggestion of nonrandom sequence variation in
RT their conserved loop-domains." RT
RL Genomics 3:59-66(1988).
RN [4]
RP SEQUENCE OF 5-702 FROM N.A.
RX MEDLINE=87128144; PubMed=3814146;
RA Oikawa S., Nakazato H., Kosaki G.;
RT "Primary structure of human carcinoembryonic antigen (CEA) deduced
RT from cDNA sequence." RT
RL Biochem. Biophys. Res. Commun. 142:511-518(1987).
RN [5]
RP SEQUENCE OF 331-702 FROM N.A.
RX MEDLINE=87204247; PubMed=3033671;
RA Zimmermann W., Ortlieb B., Friedrich R., von Kleist S.;
RT "Isolation and characterization of cDNA clones encoding the human
RT carcinoembryonic antigen reveal a highly conserved repeating
RT structure." RT
RL Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Found in adenocarcinomas of endoderally
CC derived digestive system epithelium and fetal colon.
CC -1- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 kDa
CC COMPRISING 60% CARBOHYDRATE.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like domains.
CC -1- DATABASE: NAMB=PRO; NOTE=CD guide CD66e entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd66e.htm".
CC
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45 -----VAAGETATLHCTVTSLSVPUGPIKWFKGTGPGREFIY-SQKEAPPRVTNWSDAT 97
 124 PH----ELSSISNSVALADEGEYTCSTFTMPVRTAKSL-----VTVLGHPQKPIITGYK 173
 93 KRNNDFFSIRISNITPADAGVYVCVKRKEERGDMFEKSGPGGTHLTVSAKSPVPVLSGPT 157
 174 SSUREKDTATLNCQSSGSKFA-ARLTWRKGDQBLHGEPTRIQDPPNGKTTVSSSVTFQV 232
 158 VRATPQTQVNTFTCTSGFGSPRNISLWFKNGNLSASQTSVDPEDNNVSYINSNTRKVL 217
 233 TREDDGASIVCSVNNHSLKCAD--RSTSQRIEVLVYPTAMIRPDPHPHREGOKLLHCE- 289
 218 ATGDVHSQVCEVAHVTLQGGPLRGRTANLSEIRVPPTL--EITGSFSAGNQNVVTCQV 275
 290 GRGNPVPQQVLYNEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGS----- 341
 276 NKFYPRHLQLTWLENGM-----SRTEASVYV--ENKDGTFNQTSFWLYNSSAAREAVV 328
 342 -----YKAYVTLNVDP-----SPVSSS---SYTHALIGIVAPIVIFELL 379
 329 LTCQVEHDGQPAVSKNHTLEVSAPQDKDQTGTPGPNDSNWTSTFIYVGVVCALLVALLI 388
 380 IMLIFLGHLYLRHKGYLTHERAKGSDDA-----PDADT 412
 389 AAL-----YLLRIR-----QNKAKGSTSTRLHBPENKT 417

 RESULT 13
 CL166 MOUSE
 ID CL166_MOUSE STANDARD; PRT; 583 AA.
 AC Q61490; O70136;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE CL166 antigen precursor (Activated leukocyte-cell adhesion molecule)
 DE (ALCAM) (DM-GRASP protein).
 GN ALCAM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NFS;
 RC MEDLINE=97353242; PubMed=92095000;
 RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
 RA Kobarg J., Starling G.C., Siadak A.W., Aruffo A.,
 RA "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
 RT conserved in different homologs and mediates cross-species binding.";
 RL Eur. J. Immunol. 27:1469-1478(1997).
 RN [2]
 RC SEQUENCE OF 227-583 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=94376084; PubMed=8089660;
 RA Kanki J.P., Chang S., Kuwada J.Y.;
 RT "The molecular cloning and characterization of potential chick
 RT DM-GRASP homologs in zebrafish and mouse.";
 RJ J. Neurobiol. 25:831-845(1994).
 CC -I- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
 CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
 CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
 CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
 CC THE NERVOUS SYSTEM.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -I- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC
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Matches 82; Conservative 52; Mismatches 146; Indels 63; Gaps 13;

QY 77 GGTIVLKCQV-----SSLOWNSNPAQQTLYF- 106
 DB 47 GGTIVLCHLLPPVCLYISLVTWQPDAPAHQNVAAFPKMGSPFSPKPSGSELSFV 106

QY 107 -GEKALRNRIQLVSTPHLSISINVALADEBYTCISFTMPVTRAKSLVTVLGIPIQ 165
 DB 107 SAKOSTGQTEAELODAT-----LALHGLTVEDEGNYTCEFAFPKPSGVRGM-TWLRVIA 160

QY 166 KP--IITGVKSLREKOTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPKGKFT 223
 DB 161 KPNQAEAKQVTSQDPTTVALCISKEGPPARISM-LSSLWEAKETQVSGTLAG-TVT 218

QY 224 VSSVTFTVQTRDDGASIVCSVNHSLKADRSSTORIEVLYTPTAMI-----RP 273
 DB 219 VTSRFTLVSGRADGVTVTKVHESEFE-EPALIPVTLVSRYPPEVISISGYDDNMVLRGT 277

QY 274 DPHPRREGOKLLHCHGRGNVPVQQYLWE-KGSGVPLKMTQESALIFPFLNKSQSGTVG 332
 DB 278 D-----ATLSCDVRNPEFTGTDWSTTGTFTSAVAGQSQVLIHVAVSLFNTTFV 328

QY 333 CTATSNMGSYKAYTLNVNDRPVPSSSTYHAIIGGIVAFIV 375
 DB 329 CIVTNAVGMRAEQVIFVRE-TPNTRAGATGGIIGITAAII 370

RESULT 10
 LAMP CHICK
 ID LAMP CHICK STANDARD; PRT; 338 AA.
 AC Q98919; 1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Limbic system-associated membrane protein precursor (B19S) (CHLAMP,
 DE G19-isoform).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97157768; PubMed=9004047;
 RA Wilson D.J.A., Kim D.S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
 RT "A family of glycoproteins (Gp55), which inhibit neurite outgrowth,
 RT are members of the Ig superfamily and are related to OBCAM,
 RT neurotrophin, LAMP and CEP-1".
 RL J. Cell Sci. 109:3129-3138(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97358596; PubMed=9215692;
 RA Brummendorf T., Spaltmann F., Treubert U.;
 RT "Cloning and characterization of a neural cell recognition molecule
 RT on axons of the retinotectal system and spinal cord."
 RL Eur. J. Neurosci. 9:1105-1116(1997).
 CC -!- FUNCTION: Mediates selective neuronal growth and axon targeting.
 CC Probably serves as a recognition molecule for the formation of
 CC limbic connections (By similarity).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLN
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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CC EMBL; Y08171; CAA69357.1; -
 CC EMBL; Z94720; CAB08115.1; -
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00835; IG_Like; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Lipoprotein;
 KW Membrane; GPI-anchor; Repeat; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 315
 FT LIMBIC SYSTEM-ASSOCIATED MEMBRANE
 FT PROTEIN.
 FT REMOVED IN MATURE FORM (POTENTIAL).
 FT IG-LIKE C2-TYPE 1.
 FT DOMAIN 132 214
 FT IG-LIKE C2-TYPE 2.
 FT DOMAIN 219 306
 FT IG-LIKE C2-TYPE 3.
 FT POTENTIAL.
 FT DISULFID 53 111
 FT DISULFID 153 197
 FT POTENTIAL.
 FT DISULFID 239 290
 FT POTENTIAL.
 FT LIPID 315 315
 FT GPI-anchor amidated asparagine
 FT (Potential).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 40 40
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 66 66
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 136 136
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 148 148
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 279 279
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 287 287
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 300 300
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 315 315
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 338 AA; 37394 MW; 8FA4A60AD98426B4 CRC64;

Query Match 9.9%; Score 225; DB 1; Length 338;
 Best Local Similarity 27.4%; Pred. No. 7.3e-09;
 Matches 79; Conservative 42; Mismatches 137; Indels 30; Gaps 13;

QY 62 SQDSPFTSDETVVAGTVLKCQVVDHEDSSLOWNSNPAQQTLYFGKRALDNRQLVT 121
 DB 31 SVDPTRGTDNITVRQDGTALIRCFVED-RSSKVALNL-RSGIFAGDKWSDPRVELEK 88

QY 122 STPHLSISINVALADEGEYTCISFTMPVTRAKSLVTVLGIPIQKPIITGYKSSLEKKT 181
 DB 89 RSPLEYSRIQKVVDYDEGSYTCVQTHHPTKTSQVYLIVQVPPKISINSSDITVNEGSN 148

QY 182 ATLNQSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKFTFTVSSSV--TFQVTRDDGA 239
 DB 149 VTLVCMANG-RPEVITWR-----HLTPT-----GKEFGSEEEYLILGITREQSG- 193

QY 240 STVCSVNHSLKADRSSTORIEVLYTPTAMTRPDPHPHREGOKLLHCHGRGNVPVQQY 299
 DB 194 KYECKAANE-VASAD-VKQVRVTNVYPPT-ITESKSENAATGRQALLRCEASAVPTP-DF 249

QY 300 LWEKE-----GSVPPLKMT-QESALIFPFLNKSQSGTVGCTATSNMG 340
 DB 250 EWYRDDTRINSANGLEIKTSQSLLMNVANVTEHYGNTTCVAANKIG 297

RESULT 11
 KILO RAT
 ID KILO RAT STANDARD; PRT; 348 AA.
 AC Q9Z008;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kilon protein precursor (Kindred of IgLN).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
 RX MEDLINE=99175207; PubMed=10075727;


```

FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 L -> P (IN REF. 1).
FT CONFLICT 138 138 N -> D (IN REF. 1).
FT CONFLICT 165 165 P -> PP (IN REF. 2).
FT CONFLICT 342 342 S -> G (IN REF. 3).
FT CONFLICT 428 428
SQ SEQUENCE 515 AA; 57064 MW; PFF608B5F7A0F CRC64;

Query Match
Best Local Similarity 26.2%; Score 228.5; DB 1; Length 515;
Matches 112; Conservative 59; Mismatches 153; Indels 103; Gaps 26;

QY 77 GGTVLKQVQKHEDS---SLOW---SNPAQOQLYFGEKRALDRNIQIIVTSPPHEL-- 127
Db 44 GTDVLHCSFANPLPSVKITQVTWQKASNGSKQM-----AIYPTMGVSVLPPIEKRV 97
QY 128 -----SISISNVALADEGEYTCISFTMPVRTAKSLVTLGIPQKPI--ITGYKSS 175
Db 98 EFLRPSFDIGTIRLSGLELEDEGMVYICEFATFPTGNRESQLN-LTVMAKPTNWIEGTRAV 156
QY 176 LREK---DTATL--NCOSGSGKPARLITWRKGDQELHGEPTRIO--DPNGKFTFVSSSV 228
Db 157 LRARKGQDNKVLVATCTSAANGKPPSAVSW---ETRLKGE-AEYQEIERNPG-TVTVISRY 211
QY 229 TFQVTRDDGASIVCSVNHESLKADR-STSORTEVLYTPTAMIRP-DPPHREGQKILL 286
Db 212 RLVPSEARHQSLACIVNYH---LDPRFSLTNVOYEPEVTEIGEDGNWYLORTDKL 267
QY 287 HCEGRGNVPQOYLWEK-EGSVPLPKMTQESALIP--PFLNKSDSGTYGCTATSNMGYSX 343
Db 268 TCRADANPPATEYHWITLNGSLPKGVAQNRTLPFRGP-ITYSLAGTYICEATNPIGTRS 326
QY 344 AYTLLVND-----PSP-----VPSSSTYHAIIGGIVAFIVFLIMLIFLGHYLI- 390
Db 327 GOVEVNITFPPTPTPHGRAGOMPT-----AIIQGVAGSV-----LLVLIVVGGIIVA 376
QY 391 ----RH--KGYLT-----HEAGSDPADPADTATINAEQGQS 422
Db 377 LRRRHFKGDYSYTKKHVNGYSGAGIPQHPHMAQNQLPDDSDDEKKA--SPLGSS 434
QY 423 GGDCKE 429
Db 435 YEEBEE 441

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RESULT 8

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OPCM CHICK STANDARD; PRT; 337 AA.
ID OPCM CHICK
AC Q98892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAR-2004 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Opioid binding protein/cell adhesion molecule homolog precursor
DE (Neurite inhibitor GP55-A) (OBAM protein gamma isoform).
GN OPCML.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RA Lodge A.P.; Kim D.-S.; Howard M.R.; McNamee C.J.; Smith N.; Moss D.J.;
RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBAM cDNAs from
RT chick: structural diversity of IGLON family proteins.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A.; Kim D.-S.; Clarke G.A.; Marshall-Clarke S.; Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBAM,
RT neurotmin, LAMP and CEPU-1.";
RL J. Cell Sci. 109:3129-3138(1996).
CC -!- FUNCTION: Inhibits neurite outgrowth.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -!- DEVELOPMENTAL STAGE: Increases during development from very low
CC levels at embryonic day 10 and is most abundant after hatching.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; Y08170; CAB41420.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; Igc2; 2.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Lipoprotein;
KW Membrane; GPI-anchor; Repeat; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 314
FT PROPEP 315 337 MOLECULE BINDING PROTEIN/CELL ADHESION
FT DOMAIN 32 119 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 129 211 IG-LIKE C2-TYPE 1.
FT DOMAIN 215 302 IG-LIKE C2-TYPE 2.
FT DISULFID 50 108 IG-LIKE C2-TYPE 3.
FT DISULFID 150 194 POTENTIAL.
FT DISULFID 236 288 POTENTIAL.
FT LIPID 314 314 GPI-anchor amidated asparagine
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 337 AA; 36887 MW; BAE717551856651E CRC64;

Query Match 10.0%; Score 225.5; DB 1; Length 337;
Best Local Similarity 25.4%; Pred. No. 6,7e-09;
Matches 84; Conservative 57; Mismatches 139; Indels 51; Gaps 14;

QY 73 TVVAGGTVLKCOVKHEDSLOWSNPAQOQLYFGEKRALDRNIQIIVTSPPHELSSIS 132
Db 39 TVRQGSATLRCTVDVDRV-RRVAVLN-RSTLVAGNDKWSIDNRVILSTKTQYSIKH 96
QY 133 NVALADEGEYTCISFTMPVRTAKSLVTLGIPQKPIITGYKSSLRKDTATLNCQSSGSK 192
Db 97 NVDVDEGPTCSQVQDNDNHPKTSRVHLIVQVPPQIVNISSDITVNEGSSVTLCLAPG-R 155
QY 193 PAARLTWRKGDQELHGEPTRIOEDPNKGTFTVSSSVTFQ---VTRDDGASIVCSVNHE 249
Db 156 PEPVTVWR---HLGSK-----GQGF-VSEDEYLEITGITREGSGEYCSAVNDVA 201
QY 250 LKADASTSORIEVLYPTAMIRPDPPH-----PREGQKLLHCEGRGNVPQOYLW 301
Db 202 VPDVRK---VKVTVNY-----PPYISNAKNTGASVGQKGILOCEASAVPV-AEFQW 248
QY 302 EKE-----GSVPPLKMTQE---SALIFFPLNKSDSGTYGCTATSNMGYSKAYVTLVNDP 353
Db 249 FKEDTRLANGLEGVRIESKGRSLTLTFFNVSEKDYGYNTVCTVATNKLGTNA--SIIYGP 306

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RX MEDLINE=97215901; PubMed=9062191;
 RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
 RA Ullrich A.;
 RT "A family of proteins that inhibit signalling through tyrosine kinase
 RT receptors";
 RL Nature 386:181-186(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANTS ASP-95; LEU-96; ASN-100;
 RP ARG-107; GLY-109 AND VAL-131.
 RC TISSUE=Monocytes;
 RX MEDLINE=98143722; PubMed=9485180;
 RA Brooke G.P., Parsons K.R., Howard C.J.;
 RT "Cloning of two members of the SIRP alpha family of protein tyrosine
 RT phosphatase binding proteins in cattle that are expressed on monocytes
 RT and a subpopulation of dendritic cells and which mediate binding to
 RT CD4 T cells";
 RL Eur. J. Immunol. 28:1-11(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-44; THR-50; THR-52;
 RP ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107; GLY-109 AND
 RP VAL-131.
 RC TISSUE=Brain;
 RX MEDLINE=20053880; PubMed=10585853;
 RA Sano S.-I., Ohnishi H., Kubota M.;
 RT "Gene structure of mouse BIT/SHPS-1";
 RL Biochem. J. 344:667-675(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Guilliam R., Hall R.E.,
 RA Hammond S., Harley J.B., Heath F.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levasilho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871(2001).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; THR-50;
 RP THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107;
 RP GLY-109 AND VAL-131.
 RC TISSUE=Brain, Kidney, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP FUNCTION, AND INTERACTIONS WITH FYB; SCAP2 AND PTK2B.
 RX MEDLINE=99401000; PubMed=10469599;
 RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
 RA Schraven B., Neel B.G.;
 RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
 RT multi-protein complexes in macrophages";
 RL Curr. Biol. 9:927-930(1999).
 RN [8]
 RP PHOSPHORYLATION BY JAK2, AND INTERACTIONS WITH PTPN11 AND JAK2.
 RX MEDLINE=20428742; PubMed=10842184;
 RA Stofega M.R., Argetsinger L.S., Wang H., Ullrich A., Carter-Su C.;
 RT "Negative regulation of growth hormone receptor/JAK2 signaling by
 RT signal regulatory protein alpha";
 RL J. Biol. Chem. 275:28222-28229(2000).
 RN [9]
 RP FUNCTION, AND INTERACTION WITH CD47.
 RX MEDLINE=21400825; PubMed=11509594;
 RA Latour S., Tanaka H., Demeure C., Mateo V., Rubio M., Brown E.J.,
 RA Malszewski C., Lindberg F.P., Oldenborg A., Ullrich A.,
 RA Bellespese G., Sarfati M.;
 RT "Bidirectional negative regulation of human T and dendritic cells by
 RT CD47 and its cognate receptor signal-regulator protein-alpha:
 RT down-regulation of IL-12 responsiveness and inhibition of dendritic
 RT cell activation";
 RL J. Immunol. 167:2547-2554(2001).
 CC -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
 CC as docking protein and induces translocation of PTPN6, PTPN11 and
 CC other binding partners from the cytosol to the plasma membrane.
 CC Supports adhesion of cerebellar neurons, neurite outgrowth and
 CC Gli1 cell attachment. May play a key role in intracellular
 CC signaling during synaptogenesis and in synaptic function (By
 CC similarity). Involved in the negative regulation of receptor
 CC tyrosine kinase-coupled cellular responses induced by cell
 CC adhesion, growth factors or insulin. Mediates negative regulation
 CC of phagocytosis, mast cell activation and dendritic cell
 CC activation. CD47 binding prevents maturation of immature dendritic
 CC cells and inhibits cytokine production by mature dendritic cells.
 CC -!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
 CC macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
 CC Binds FGR (By similarity). Binds JAK2 irrespective of its
 CC phosphorylation status and forms a stable complex. Binds SCAP1
 CC and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=P78324-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P78324-2; Sequence=VSP_007030;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=P78324-3; Sequence=VSP_007029;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
 CC Detected on myeloid cells, but not T cells. Detected at lower
 CC levels in heart, placenta, lung, testis, ovary, colon, liver,
 CC small intestine, prostate, spleen, kidney, skeletal muscle and
 CC pancreas.
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: Phosphorylated on tyrosine residues in response to
 CC stimulation with EGF, growth hormone, insulin and PDGF.
 CC Dephosphorylated by PTPN11.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.

CC CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/2005693930_g.htm".

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CC CC -----

DR ENBL; X76400; CAA53980.2; ALT_INIT.

DR ENBL; AF060231; AAC23798.1; -.

DR ENBL; AY029539; AAK33124.1; -.

DR ENBL; AF252867; AAG16648.1; -.

DR ENBL; AF196768; AAG16648.1; JOINED.

DR ENBL; AF196769; AAG16648.1; JOINED.

DR ENBL; AF196770; AAG16648.1; JOINED.

DR ENBL; AF196771; AAG16648.1; JOINED.

DR ENBL; AF196774; AAG16649.1; -.

DR ENBL; AF196768; AAG16649.1; JOINED.

DR ENBL; AF196769; AAG16649.1; JOINED.

DR ENBL; AF196770; AAG16649.1; JOINED.

DR ENBL; AF196771; AAG16649.1; JOINED.

DR ENBL; AF196772; AAG16649.1; JOINED.

DR ENBL; AF196773; AAG16649.1; JOINED.

DR GENE; HGNC:9706; PVRL1.

DR MIM; 600644; -.

DR MIM; 225000; -.

DR MIM; 225060; -.

DR GO; GO:0016021; C:integral to membrane; NAS.

DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.

DR GO; GO:0015026; F:coreceptor activity; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; ig; 2.

DR SMART; SMO0406; IGv; 1.

DR PROSITE; PS00835; IG_LIKE; 2.

CC CC Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;

KW Repeat; Glycoprotein; Signal; Alternative splicing.

FT SIGNAL 1 30

FT CHAIN 31 517

FT DOMAIN 31 355

FT TRANSMEM 356 376

FT DOMAIN 377 517

FT DOMAIN 31 141

FT DOMAIN 149 238

FT DOMAIN 247 334

FT DOMAIN 437 444

FT DOMAIN 445 449

FT DISULFID 51 124

FT DISULFID 172 226

FT DISULFID 269 316

FT CARBOHYD 36 316

FT CARBOHYD 72 72

FT CARBOHYD 139 139

FT CARBOHYD 202 202

FT CARBOHYD 286 286

FT CARBOHYD 297 297

FT CARBOHYD 307 307

FT CARBOHYD 332 332

FT VARSPLIC 335 352

FT (in isoform Gamma).

FT Missing (in isoform Gamma).

FT /FTid=Vsp_002625.

FT PVPYTPPEHGRAGPVPTAIGVAGSILLVLIVGVIV

FT ALRRRHTFKGDYTKKHVYNGSKAGIPQHHPMAQNLQ

FT YPDSDDKKAGPLGGSSSEEEEEEGGGGGRKVGPH

FT -> KRPQRLGSLAARLAVTLVAVLVVFFLYNRQ

FT QKSPETDAGCTDPLSOKPEPSRQSLVPEDIQVHLD

FT PGRQQQEEEDLQKLSQPPYDILGVSPSYHPSVRRTEPRG

FT ECP (in isoform Alpha).

FT VARSPLIC 459 517 /FTid=VSP_002626.

FT Missing (in isoform Alpha).

FT /FTid=VSP_002627.

SQ SEQUENCE 517 AA; 57158 MW; DF34C8AEC93BE6D CRC64;

Query Match 10.6%; Score 239; DB 1; Length 517;

Best Local Similarity 26.8%; Pred. No. 1.3e-09;

Matches 114; Conservative 52; Mismatches 161; Indels 98; Gaps 24;

QY 77 GTTVLTKCQVKDEHS-----SLQWS-----NPAQOTLYFGKRALRDNRQL 119

Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPMSGVSLAYPR-----BRVEF 99

QY 120 VTSTPHELISISNVALADEGYTCSIFTMPVVRTAKSLVTLVILGIPQKPI--ITGYKSSLR 177

Db 100 LRPSFTDGTIRLSRLEDEGVVYCEFAFTPTGNRESQLN-LTVMAKPTNWIEGTQAVLR 158

QY 178 EK---DTATL--NCQSSGSKPAARLTWRKGDDELHCEPRTIQE--DPNGKTFVTSSSVTF 230

Db 159 AKKGQDDKVLVATCTSAANGKPPSVWSW---ETRLKGE-AYEQEIRNPNG-TVTVISRYRL 213

QY 231 QVTRDDGASIVCSVNHESILKGADR-STSORIEVLYTPTAMIRP-DPPHREGQKLLIHC 288

Db 214 VPSREAHQOSLACIVNYH---MDRFKESLTLNVQYEPVETIEGFGNWLQEMDKVLTC 269

QY 289 EGRGNVPVQOYLWEK-EGSVPLPKMTQESALIPFP-LNKSDSGTYGCTATSNNGSYKAY 346

Db 270 KADANPPATEYHWTTLNGLSKGVAQNRTLPKGPINVSAGTYICEATNPIGTRSGQV 329

QY 347 TLNVND-----PS-----PVPSSSYTHAIGGIVAFIVFELLIMLIFLGHYLL--- 390

Db 330 EVNITEFPYTPSPPEHRRAGPVPT-----AIIIGVAGSI-----LLVLIVVGIVVALR 379

QY 351 --RH--KGTVLT-----HEAKGSDDAPDADTAIINAEGOSGG 424

Db 360 RRHRTFGDYSTKHYVNGYSKAGIPQHHPMAQNLQYPPDSDDEKKA--GFLGSSSYE 437

QY 425 DDKE 429

Db 438 EEEEE 442

RESULT 6

SHSI_HUMAN STANDARD; PET; 503 AA.

ID P78324; O00683; O43799; Q8N517; Q8TAL8; Q9H022; Q9UDX2; Q9UIJ6;

AC Q9V4U9;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor

DE (SHP substrate-1) (SHPs-1) (inhibitory receptor SHPS-1) (Signal-

DE regulatory protein alpha-1) (SHP-alpha-1) (SHP-alpha-2) (SHP-alpha-

DE 3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based

DE activation motifs) (Bit) (Macrophage fusion receptor) (p84).

GN PFNSI OR SHPSI OR SIRP OR MYD1 OR BIT OR MFR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=97223399; PubMed=9070220;

RA Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,

RA Fujioka Y., Kasuga M.;

RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal

RL localization of genes.";

RN Blochem. Biophys. Res. Commun. 231:61-67 (1997).

RP [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), POLYMORPHISM, PHOSPHORYLATION,

RP N-GLYCOSYLATION, AND INTERACTIONS WITH PTFN11, PTFN6 AND GRB2.

RC TISSUE=Placenta;

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CC -----

DR EMBL: AF308632; AAC30281.1; -
DR HSP: P06907; INEU
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 443 POLY-GLY.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 11.1%; Score 250.5; DB 1; Length 515;
Best Local Similarity 26.9%; Pred. No. 2e-10;

Matches 116; Conservative 54; Mismatches 157; Indels 105; Gaps 25;

QY 77 GGTIVLKCQKDH-----EDSSLOW-----NPAQQLYFGEKRALDRRIQL 119
DB ||||| : : : : : |||||
DB 44 GTDVLHCFANPLPGVKITQVTWQKATNGSKQVAINPAMGVSLAPYR-----ERVEF 99
QY 120 VTSSTPHELSTISINVALADEGYTCSTFTMPVPTAKSLVTLVGIPOKPI---ITGYKSLR 177
DB ||||| : : : : : |||||
DB 100 LRPSFTDGTIRLSRLLEDEGVYICFATFPAGNRBSQLN-LTWMAKPTNWIETQAVLR 158
QY 178 E---KDTATL--NCQSGGKPAARLTWRKQDQELHGEPTRIQE--DPNGKTFVTSSSVTF 230
DB ||||| : : : : : |||||
DB 159 AKGKDKKVLVATCTSANGKPPSVSN---ETHLKE-AYEQIRPNPG-TVTVISRYRL 213
QY 231 QVTREDDGASIVCSVNHSLKQADR-STQRIEVLTYPTAMIRP-DPPHPREQKLLHC 288
DB ||||| : : : : : |||||
DB 214 VPSREDHROSACIVNH-----MDRPRESLTNVQVEPEVTIEGFGNWWYLRQMDVKLTC 269
QY 289 EGRGNFVPOQYLWEK-EGSVPLPKMTQESALIF--PFLNKSDSGTGCTATSNMGYSKAY 345
DB ||||| : : : : : |||||
DB 270 KADANPPATEYHWTTLNGLSLFKGVEAQNRTLFFRGP-INYSMAGTYICATNPIGTRSG 328
QY 346 YTLNVND-----PSP-----VPSSSSTYHAIIGGIIVAFIVFLLLIMLIFLGHYLI-- 390
DB ||||| : : : : : |||||
DB 329 VEVNIETFPPTPPPEHGRAGQVPT-----AIIQGVGSI-----LLVLVVGVGVVAL 378
QY 391 ---RH--KGYLTHE-----AKGSDP-----APDADTAIIN 416
DB ||||| : : : : : |||||
DB 379 CRRRHTFKGDYSTKHHVYNGYSKAGIPQHPHPPMAQLQVPEDSDDEKKAPLGGSYYE 438
QY 417 AEGGQSGGDDKK 428
DB ||||| : : : : : |||||

Db 439 EBEEGGGGERK 450
RESULT 5
PVRI_HUMAN
ID PVRI_HUMAN STANDARD; PRT; 517 AA.
AC Q15223; O75465; O9HB36; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD111 antigen).
GN PVRL1 OR PRR1 OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "cDNA characterization and chromosomal localization of a gene related
RT to the poliovirus receptor gene.";
RL Gene 155:261-265(1995).
RN [2]
SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127;
RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
RA Spear P.G.;
RT "Entry of alphaherpesvirus mediated by poliovirus receptor-related
RT protein 1 and poliovirus receptor.";
RL Science 280:1618-1620(1998).
RN [3]
SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
RA Campadelli-Fiume G., Dubreuil P.;
RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
RT nectin1 (or prr1-highvrec) modulates positively and negatively
RT susceptibility to hsv infection.";
RL J. Virol. 75:5684-5691(2001).
RN [4]
SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
RX MEDLINE=20392396; PubMed=10932188;
RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
RA Helms J.A., Spritz R.A.;
RT "Mutations of PVRL1, encoding a cell-cell adhesion
RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
RT dysplasia.";
RL Nat. Genet. 25:427-430(2000).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAPERPVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoform gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Delta;
CC IsoId=Q15223-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
CC Name=Gamma;
CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
CC ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is
CC responsible for allelic forms known as Margarita Island ectodermal
CC dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);

DR EMBL; X64118; CAA45478.1; JOINED.
 DR EMBL; X64119; CAA45478.1; JOINED.
 DR EMBL; X64120; CAA45478.1; JOINED.
 DR EMBL; X64121; CAA45478.1; JOINED.
 DR EMBL; X64122; CAA45478.1; JOINED.
 DR EMBL; X64123; CAA45478.1; JOINED.
 DR EMBL; X64116; CAA45479.1; JOINED.
 DR EMBL; X64117; CAA45479.1; JOINED.
 DR EMBL; X64118; CAA45479.1; JOINED.
 DR EMBL; X64119; CAA45479.1; JOINED.
 DR EMBL; X64120; CAA45479.1; JOINED.
 DR EMBL; X64121; CAA45479.1; JOINED.
 DR EMBL; X64122; CAA45479.1; JOINED.
 DR EMBL; X64123; CAA45479.1; JOINED.
 DR EMBL; X64116; CAA45480.1; JOINED.
 DR EMBL; X64117; CAA45480.1; JOINED.
 DR EMBL; X64118; CAA45480.1; JOINED.
 DR EMBL; X64119; CAA45480.1; JOINED.
 DR EMBL; X64120; CAA45480.1; JOINED.
 DR EMBL; X64121; CAA45480.1; JOINED.
 DR EMBL; X64122; CAA45480.1; JOINED.
 DR EMBL; X64123; CAA45480.1; JOINED.
 DR EMBL; AC068948; AAF69803.1; --
 DR PIR; A43024; RWHUPD.
 DR PIR; S12048; RWHUPA.
 DR Genew; HGNC:9705; PVR.
 DR MIM; 173850; --
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007125; P:invasive growth; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 Repeat; Antigen; Alternative splicing; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT POTENTIAL
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 105 105
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 218 218
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT VARSPPLIC 340 384
 FT VARSPPLIC 331 331
 FT VARSPPLIC 332 384
 FT VARSPPLIC 385 392
 FT VARSPPLIC 393 417
 FT VARIANT 67 67
 FT VARIANT 340 340
 FT SEQUENCE 417 AA; 45302 MW; D15C012CE853169B CRC64;

Query Match 11.6%; Score 263; DB 1; Length 417;
 Best Local Similarity 25.7%; Pred. No. 2e-11;
 Matches 108; Conservative 50; Mismatches 158; Indels 104; Gaps 17;
 QY 5 AASLLLLLLFACCAAGGANSODGYWQEQDLELGTILAPLDEAISTVWSSPDMLASQD 64
 DB |||||
 QY 65 SQTPTSDETVA-----GGTVLKC--QVKDHE--DSSLOWSNPAQOTLYFGEKRA 111
 DB |||||
 QY 24 --PGTGVVVOAPTQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWAR-----HGEGSG 74
 DB |||||
 QY 112 L-----RDNRIQLVTSFHELSISINVA-----ADSGEYTCSTFTMPVR 152
 DB |||||
 QY 75 MAVFHTQGPSYSESKLEFVA--RLGAELRNASLRMFLGRVEDEGNYTCLFVTFP-Q 130
 DB |||||
 QY 153 TAKSLTVLGIPOKPIITG--YKSLREKDTATLNCSSGSKPAARLTWRKGDOLHCEP 210
 DB |||||
 QY 131 GSRSDIWLRLAKPONTAEVQKVLAGEVPVPMARCVSTGGRPPAQITWH---SDLGMP 187
 DB |||||
 QY 211 TRIQEDN--GKTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIVELYTPT 268
 DB |||||
 QY 188 NTSQV--PGFLSGTIVTSLMILVPSQVDGKNVTCKVEHSEFKPQLT-VNLTVYYPE 245
 DB |||||
 QY 269 AMIRPDPPHPREGQ-KLLHCEGRGNPVPQYLWEKE-GSVVPLKMTQESALIFPFLNKS 326
 DB |||||
 QY 246 VSIQYDNNWYLGQNEATLTCDAENPEPTGYNNWSTMTGMLPPFAVQAQQLIRPVDPK 305
 DB |||||
 QY 327 DSGTYGCTATSNMGSKYAYTLNVDSPVSSSTYHAIGTVAFIVFLLIMLIFLG 386
 DB |||||
 QY 306 INTTLICNVTNALGARQALTVQKGPSPSEHSGISRNAII-----FLVLGLVFLILG 360
 DB |||||

RESULT 3

PVR2 MOUSE

ID PVR2 MOUSE STANDARD; PRT; 530 AA.
 AC P32507; Q62096;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
 entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
 GN PVRL2 OR PVS OR PVR OR MPH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=92219365; PubMed=1560525;
 RA Morrison M.E., Racaniello V.R.;
 RT "Molecular cloning and expression of a murine homolog of the human
 poliovirus receptor gene.";
 RL J. Virol. 66:2807-2813 (1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=C57BL/6; Tissue=Brain;
 RX MEDLINE=94179228; PubMed=8132569;
 RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
 RT "Amino acid residues on human poliovirus receptor involved in
 interaction with poliovirus.";
 RL J. Biol. Chem. 269:8431-8438 (1994).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=FVB/N; Tissue=Colon;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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DR PROSITE; PS0835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 85 85
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VARSPLIC 386 392
FT VARSPLIC 393 417
FT VARSPLIC 417 AA; 45464 MW; DA4AD0FE4D2F6B1F CRC64;
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6B1F CRC64;

Query Match 12.0%; Score 272; DB 1; Length 417;
Best Local Similarity 26.2%; Pred No. 4.5e-12;
Matches 106; Conservative 56; Mismatches 183; Indels 60; Gaps 16;

QY 67 PWTSDETVVA-----GGTVVLKC--QVKDHE-----SSIQSNPAQ-----QT 103
Db 24 PGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSLTWSRHGSGSMVAFHQTQ 83

QY 104 LYFGEKALRDNRQLQVTSFHELSISISVALADEGEYTCSTFTMPVRAKSLVTVGI 163
Db 84 PNYSEPKRLEFVAARLGTTEL-RDASLRFGLRVEDEGNYTCLFVTFP-QGSRSDVILWRV 141

QY 164 PQKPIITG--YKSLREKDTATLNCQSSGSKPAARLTWRKQDQLHGEPTRIQEDPN--G 219
Db 142 LAKPONTAEQVKQVLTGKFPVAVKCVSTGGRPPAHITWH---SDLGMPNTSQA-PGFLS 197

QY 220 KTFVTSSVTFQVTRDDGASIVCSNVHESLKGADRTSQRIEYLYTFTAMIRP-DPPHP 278
Db 198 GTVTVTSLWILVPSQVDGKSVTKVHEHSPEKPOLLT-VNLTVYYPEVSIQSYDNNWY 256

QY 279 REGOKLLHCEGRNPVPQVLYEKE-GSVPLKMTQESALIFPFLNKSQSGTYGCTATS 337
Db 257 LSQNEATLTCDARENPEPTGYNWSTTWGPPFPFVAQAQALLIRPDKPINTTFICNVTN 316

QY 338 NMGSYKAYTINVND-PSPVPSSSTYHAIIGGIVAFIVFLLIMLIFLG----- 386
Db 317 ALGARQAEIVQVKEGPPSPSGNSS-----NIIILIGVILLTLLIGLYFYRSRC 370

QY 387 -----HYLRHKGTVLTHAKSGDDADPADTAINAEQGQSG 424
Db 371 SREFLWCHLSPSSEEHASASANGYISYSDVSRREASSQDPQTEG 415

RESULT 2
PVR_HUMAN
ID PVR_HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;

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RN RP SEQUENCE FROM N.A.
RX MEDLINE=89186426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
sequence, and expression of a new member of the immunoglobulin
superfamily.";
RL Cell 56:855-865(1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=9106015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RT Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
and secreted forms.";
RL EMBO J. 9:3217-3224(1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyanni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RT Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT "Sequence analysis of a 1mb region in 19q13.2 containing a zinc finger
gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N Glycosylation of the virus binding domain is not essential for
function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS.
CC Event-alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24407; AAA36461.1; --
CC EMBL; M24406; AAA36462.1; --
CC EMBL; X64116; CAA45478.1; --
CC EMBL; X64117; CAA45478.1; JOINED.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 9.17522 Seconds
(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187b-8

Perfect score: 2264

Sequence: 1 MGAPASLLLLLLLACFWA.....ALINAEQGSGDDKKEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	12.0	417	1	PVR_CERAE
2	263	11.6	417	1	PVR_HUMAN
3	256	11.3	530	1	PVR2_MOUSE
4	250.5	11.1	515	1	PVR1_PIG
5	239	10.6	517	1	PVR1_HUMAN
6	238.5	10.5	503	1	SHS1_HUMAN
7	228.5	10.1	515	1	PVR1_MOUSE
8	225.5	10.0	337	1	OPCM_CHICK
9	225.5	10.0	538	1	PVR2_HUMAN
10	225	9.9	338	1	LAMP_CHICK
11	220.5	9.7	348	1	KILO RAT
12	217.5	9.6	506	1	SHS1_BOVIN
13	217.5	9.6	583	1	C166_MOUSE
14	216.5	9.6	702	1	CEA5_HUMAN
15	215	9.5	739	1	VCAL_RAT
16	212.5	9.4	583	1	C166_HUMAN
17	212	9.4	4391	1	PGBM_HUMAN
18	208	9.2	345	1	OPCM_HUMAN
19	207	9.1	345	1	OPCM_HUMAN
20	206	9.1	509	1	SHS1_RAT
21	205.5	9.1	338	1	LAMP_RAT
22	205	9.1	338	1	LAMP_HUMAN
23	205	9.1	344	1	NTRI_HUMAN
24	204	9.0	513	1	SHS1_MOUSE
25	203	9.0	345	1	OPCM_BOVIN
26	198.5	8.8	353	1	CEPU_CHICK
27	197.5	8.7	547	1	ICAC_HUMAN
28	197	8.7	344	1	NTRI_MOUSE
29	196	8.7	344	1	NTRI_RAT
30	196	8.7	3707	1	PGBM_MOUSE
31	192.5	8.5	1051	1	PTK7_CHICK
32	192.5	8.5	1447	1	DCC_MOUSE
33	191.5	8.5	1443	1	NEOI_CHICK

34	191	8.4	764	1	ICCR_DROME	Q08180 drosophila
35	190.5	8.4	555	1	CL66_CARAU	Q90304 carassius a
36	188	8.3	3375	1	UN52_CABEL	Q06561 caenorhabdi
37	187.5	8.3	588	1	CL66_CHICK	P42292 gallus gall
38	184	8.1	1377	1	NEOI_RAT	P97603 rattus norv
39	183	8.1	403	1	RAGE_MOUSE	Q62151 mus musculu
40	182.5	8.1	628	1	LU_HUMAN	P20895 homo sapien
41	181	8.0	387	1	SRE2_HUMAN	Q9PIW8 homo sapien
42	180.5	8.0	564	1	CL66_BRARE	Q90460 brachydanio
43	179.5	7.9	499	1	SIL8_HUMAN	Q9NYZ4 homo sapien
44	179	7.9	344	1	CEA6_HUMAN	P40199 homo sapien
45	178	7.9	1241	1	NPHN_HUMAN	O60500 homo sapien

ALIGNMENTS

RESULT 1

PVR_CERAE
ID PVR_CERAE STANDARD; PRT; 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059631; PubMed=1331508;
RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
has no putative N-glycosylation site in the functional N-terminal
immunoglobulin-like domain.";
RL J. Virol. 66:7059-7066(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like_v-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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or send an email to license@isb-sib.ch).

EMBL; D12611; BAA02136.1; -;
DR EMBL; D12612; BAA02137.1; -;
DR PIR; A44194; A44194.
DR PIR; B44194; B44194.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.

Job time : 14.4885 secs

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Db 474 AEDTGKALVCLAKLHSSOMSEPKQKQSTQTLVYNNAPKEPTIWVSPSPV-PEEGSPVNL 532
Qy 287 HCEGRGNVPQOYLWE---KEGSVEPLKMTQESALIFPFLNKSQSGTYGCTATNMGSYK 343
Db 533 TCSSDGFPTP-KILWSRQLKNGELQPL--SQNTTSLFNATKMGDSGIYVCEGINEAGISK 589
Qy 344 AYYTLNVNDPS-----PVPSSSTYHAIIG--GIVAFIVFL-----LIMLIF 384
Db 590 KVELLIHQSSKDIQLTVFPKSKVKEGTVIISCTCGSVPEIWIILKKAKTGDWVLKSV 649
Qy 385 LGHYLIR-----HKGTY-----LTHEAKGSDDAPD-----ADTAI 414
Db 650 NGSYTIRKAQLQDAGVCECKTEVGSQLSRLTLDVKGKNNKDYFSPPELLALYFASSLV 709
Qy 415 INAEG 419
Db 710 IPAIG 714

RESULT 15
153960
PRR2 alpha - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C:Accession: I53960
R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I53960
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-478 <RES>
A:Cross-references: GB:S79171; NID:g1042202; PID:g1042203
C:Genetics:
A:Gene: PRR2alpha
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 9.4%; Score 213.5; DB 2; Length 478;
Best Local Similarity 22.7%; Pred. No. 1.3e-07;
Matches 89; Conservative 55; Mismatches 167; Indels 81; Gaps 16;

Qy 77 GGTVVLKQV-----KDHE-----SSLOWNPAAQOTLYF- 106
Db 47 GGTVELCHLLPPVPGLYISLVTWQRDPANQHVAAAFPKMGPPSPKPGSERLSFV 106
Qy 107 -GEXRALDRNRQLVSTPHELISISNVALADEGEVTCSTFTMPVRTAKSLVTVLGIQ 165
Db 107 SAKQSTGQDTEAEHQDAT-----LALHGLTVEDEGNYTCFATFPKGSVRGM-TWLRVIA 160
Qy 166 KP--IITGYKSLREKDTATLNCQSSGSKPAARLTWRKQDELHCEPTRIQEDPNGKFTT 223
Db 161 KPKNQAEAKQVTFQSDPTTVALCISKEGRPPARISW-LSSLDWEAKETQVSGTLAG-TVT 218
Qy 224 VSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTMT-----RP 273
Db 219 VTSRFTLVPSGRADGVTVTCVKEHESFE-EPALIPVTLVSVRYPEVSISSGYYDDNWLGR 277
Qy 274 DPPHPREGQKLLHCEGRGNPVPQOYLWE-KEGSVPPPLKMTQESALIFPFLNKSQSGTYG 332
Db 278 D-----ATLSCDVRNPEPTGYDWSITTSFTPSAQAQGSQVVIHAVDSLFTNTFV 328
Qy 333 CTATSNMGSYKAYTLNVND-PSVPSSSSTYHAIIGIVAFIVFLIMLIFLGHYLIR 391
Db 329 CTVTNAVGMGRAEQVIFVRETPRRDRVGPLVWGAAGV-----TLVLILLAGGSL-- 379
Qy 392 HKGYLTHEAKGSDDAPDADTAIINAEQGSG 423
Db 380 ---AFILLVRRRRKSPG-----GAGGASG 402
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Search completed: May 27, 2004, 09:32:26

QY 224 VSSSVTFQVTRDDGASIVCSVNHE-----LKGADRTSQRIEVLTYPTAMIRPDP 275
 Db 3535 --SHITINKAKLSGGKGYICRASNEAGTSDIDLILKILVPPKIDKSNIGNPLAIV---- 3588
 QY 276 PHPRGQKLLHCHGRGNVPVQQYLWEKESVPLKMTQBSALIFPFLNK-----S 326
 Db 3589 -----ARTYLECPISGIPQP-DVIWTKNGM--DINMT-DSRVILAQNNETFGIENVQVT 3639
 QY 327 DSGTYGCTATSNMGSKYKAYTYTLNVNDP 353
 Db 3640 DQGRYCTATNRGKGKASHDFSLDLVSP 3666
 RESULT 12
 T43290
 hemiscitin precursor - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43290; T20993; T24734
 R:Vogel, B.E.; Hedgecock, E.M.
 A:Description: Hemiscitin is required for hemidesmosome mediated cell adhesion and germ-
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z23396
 A:Accession: T43290
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-5198 <VOG>
 A:Cross-references: EMBL:AF074901; PIDN:AAC26792.1
 R:Sulston, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19355
 A:Accession: T20993
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <WIL>
 A:Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CBSP:F15G9.4b
 A:Experimental source: clone F15G9
 R:Kershaw, J.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: Z19929
 A:Accession: T24734
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <W12>
 A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CBSP:F15G9.4b
 A:Experimental source: clone T09B9
 C:Genetics:
 A:Gene: him-4; F15G9.4b
 A:Map position: X
 A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
 ; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;
 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1
 Query Match 9.6%; Score 217; DB 2; Length 5198;
 Best Local Similarity 24.5%; Pred. No. 1.7e-06;
 Matches 80; Conservative 57; Mismatches 124; Indels 66; Gaps 15;
 QY 55 SSPDMLASQDSQPWTSDETV-----VAGGTIVLKQVKDHDSSLOWNPAAQOTLYFGE 108
 Db 3378 SEQDFKNVYTKPI-DETIDQPKAVAGGEIILKCPVLGNPTVTWKR-----GD 3428
 QY 109 KRALRDRRIQLVSTPHELSISISNVALADEGYTCISFTMPVTRAKSLVT-----VLGI 163
 Db 3429 DAVPNDSRHRTIV-----NNYDLKINSVTTEDAGQVSC-----IAYNEAGNLTHYAAEVIGK 3480
 QY 164 PQKPIITGYKSSLRKQDTATLNCSSGSKPAALTWKRGDQELHGEPTRIQEDPNGKTF 223
 Db 3481 PTFVRKGNLYEVIENDTITMDCGVT-SRPLPSISWFRGDKPY-LYDRVISISPDG---- 3534
 QY 224 VSSSVTFQVTRDDGASIVCSVNHE-----LKGADRTSQRIEVLTYPTAMIRPDP 275
 Db 3535 --SHITINKAKLSGGKGYICRASNEAGTSDIDLILKILVPPKIDKSNIGNPLAIV---- 3588

QY 276 PHPRGQKLLHCHGRGNVPVQQYLWEKESVPLKMTQBSALIFPFLNK-----S 326
 Db 3589 -----ARTYLECPISGIPQP-DVIWTKNGM--DINMT-DSRVILAQNNETFGIENVQVT 3639
 QY 327 DSGTYGCTATSNMGSKYKAYTYTLNVNDP 353
 Db 3640 DQGRYCTATNRGKGKASHDFSLDLVSP 3666
 RESULT 13
 A36319
 carcinoembryonic antigen precursor - human
 N:Alternate names: CEA; meconium antigen 100
 C:Species: Homo sapiens (man)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000
 C:Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098; A26
 R:Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shively,
 Mol. Cell. Biol. 10, 2738-2748, 1990
 A:Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its prom
 A:Reference number: A36319; MUID:90258861; PMID:2342461
 A:Accession: A36319
 A:Molecule type: DNA
 A:Residues: 1-702 <SCH>
 A:Cross-references: GB:M17303; NID:G178676; PIDN:AAB59513.1; PID:G178677
 A:Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-Thr
 R:Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
 Mol. Cell. Biol. 7, 3221-3230, 1987
 A:Title: Isolation and characterization of full-length functional cDNA clones for human
 A:Reference number: A27773; MUID:88038876; PMID:3670312
 A:Accession: A27773
 A:Molecule type: mRNA
 A:Residues: 1-702 <BEA>
 A:Cross-references: GB:M29540; NID:G180222; PIDN:AAA51967.1; PID:G180223
 R:Barnett, T.; Goebel, S.J.; Notthdurft, M.A.; Elting, J.J.
 Genomics 3, 59-66, 1988
 A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
 A:Reference number: A31037; MUID:89122014; PMID:3220478
 A:Accession: A31037
 A:Molecule type: mRNA
 A:Residues: 1-702 <BAR>
 A:Cross-references: GB:M29540; NID:G180222; PIDN:AAA51967.1; PID:G180223
 A:Note: the authors translated the codon GTG for residue 130 as Leu
 R:Oikawa, S.; Nakazato, H.; Kosaki, G.
 Biochem. Biophys. Res. Commun. 142, 511-518, 1987
 A:Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
 A:Reference number: A25845; MUID:87128144; PMID:3814146
 A:Accession: A25845
 A:Molecule type: mRNA
 A:Residues: 5-702 <OIK>
 A:Cross-references: GB:M15042; NID:G180198; PIDN:AAA51963.1; PID:G180199
 R:Oikawa, S.
 submitted to the EMBL Data Library, September 1989
 A:Reference number: S08106
 A:Accession: S08106
 A:Molecule type: mRNA
 A:Residues: 5-319,321-702 <OIK>
 A:Cross-references: EMBL:X16455; NID:G29854; PIDN:CAA34474.1; PID:G825638
 R:Barnett, T.
 submitted to the EMBL Data Library, September 1991
 A:Description: Genomic DNA sequence upstream of the translational start of the carcinoem
 A:Reference number: S31737
 A:Accession: S31737
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-141 <BA2>
 A:Cross-references: EMBL:X62151
 R:Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A:Title: Identification of three new genes and estimation of the size of the carcinoembr
 A:Reference number: A44476; MUID:93052339; PMID:1427854
 A:Accession: A44476
 A:Status: preliminary; not compared with conceptual translation

Db 100 LRPFTDGTIRLSLEUDEGVYICEFATFTPGNRESQLN-LTVNAKPNTNWIEGTOAVLR 150

Qy 178 EK---DTATL--NCQSNGSKFAARLTWRKGDELHCEPTRIQEDPNG-KTFTVSSSVTF 230

Db 159 AKKGDDKVLVATCTSANGKEPSVSWS---ETRLKGE-ARVPDGSGTPMAPVTVISRYEL 214

Qy 231 QVTRDDGASIVCSVNHSLSKGAER-STSQRIEVLVTTAMIRP-DPPHPREGQKILLHC 288

Db 215 VPSREAHQQSLACIENVYH---MDRFKESILNVQYEPEVTIEGFDGNWYLQRMVDVKLC 270

Qy 289 EGRGNPVPOQVILEK-EGSVPLPKMTQESALIFPF-LNKSDSGTTCGCTATSNMGSYKAY 346

Db 271 KADANPPATEYHTWTTLINGSLPKGVEAQNRITLFFKGINYSLAGTYICBATNPIGTRSQGV 330

Qy 347 TLNVND----PS-----PVSSSTSYHAIIIGGIVAFTVFELLMLFLIGHVLI--- 390

Db 331 EVNLITEFPYTPSPPEHGRRACGPVT-----AIIIGVAGSI:::|::|::|:: 380

Qy 391 --RH--KGYLYT-----HEAKGSDAPDADTAITINAEQGSGG 424

Db 381 RRRRTFKGDYSTKKHVYNGYGSKAGIQPHHPMAQNLOYPDSDDDEKA--GPLGGSSYE 438

Qy 425 DDKKE 429

Db 439 EEEEE 443

RESULT 11

T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T20992; T24733
R/Sulston, J.
submitted to the EMBL Data Library, December 1994

A/Reference number: Z19355
A/Acession: T20992
A/Status: preliminary; translated from GE/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-5175 <WL>
A/Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CBSP:F15G9.4a
A/Experimental source: Clone F15G9
R/Kershaw, J.
submitted to the EMBL Data Library, December 1994

A/Reference number: Z19929
A/Acession: T24733
A/Status: preliminary; translated from GE/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-5175 <WI2>
A/Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CBSP:F15G9.4a
A/Experimental source: Clone T09B9
C/Genetics:
A/Gene: CBSP:F15G9.4a
A/Map position: X
A/Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3/3/ 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 494/1; 5011/

Query Match 9.6%; Score 217; DB 2; Length 5175;
Best Local Similarity 24.8%; Pred. No. 1.7e-06;
Matches 80; Conservative 57; Mismatches 124; Indels 66; Gaps 15;

Qy 55 SSPDMLASQSQWTSDET-----VAGTGTVLKQCVKDHDSSLOWSNPAQOTLVFG 108

Db 3378 SEQDFKNVYTKBYI-DEIIDQTPKAVAGEIILKPVLGNNPTVTWKR-----GD 3428

Qy 109 KRALRNRLQLTSTSTPHEUSISISNVALADEGYTCSIFTMPVRTAKSLVT-----VLGI 163

Db 3429 DAVPNDSRRTIV-----NNYDLKINSVTTEDAQVSC-----IAVNEAGNLTHYAAREVIGK 3480

Qy 164 PQKEPIITGYKSSLREKQDTATLNQCSSGSKPAARLTWRKGDELHCEPTRIQEDPNKGTFT 223

Db 3481 PTFVRKGNGLYEVIENTITMDCGV-SRELPSISWFRGDKPYV-LYDRYSISPDG--- 3534

Db 60 TTERVSQVTWORLD-----GTVV-----AAHPSPGVDFPN----- 90
 QY 105 YFGEKRALDRNIQOLVSTP-----HELSSISNVALADGEVTCSTFTMPVETAKSLV 158
 Db 91 -----SQFSKDLRFVARPETNADRLDRLAFLRGLRVEDGNTCTCFATFNGTRRG-V 144
 QY 159 TVLGIPOKP--IITGYKSSUREKDTATLNCOSGSKFAARLTWRKQDLHGEPTRIQED 216
 Db 145 TMLRVIAOPENHAEAEQVETIGTQSVAVARCVSTGGRPPARITW---ISSLGEAKDQEP 201
 QY 217 P-NGKTTVSSVTFQVTRDDGASIVCSVNHESLKGADRSSTORIEVLVPTTAMIRPDP 275
 Db 202 GIQAGTVIISRYSLVPVGRADGVKVTCTRVEHSEFEE-----PILLFVTLVRYPP 252
 QY 276 PHPREG-----QKLLHCEGRGNPVPQOYLWE-KEGSVPPLKMTQESALIFPLNK 325
 Db 253 EVSISGYDDNWLGRSEAILTCVRSNPEPTDYDWTSTGVPFASAVAQSQQLLVHSDVR 312
 QY 326 SDGTYGCTATNSMGSKAYITLVNDPSPVPSSSTYHAIIGGIVAFIVFLLIMLIFL 385
 Db 313 MVNTFTICTATNAVGTGRAEQVILVRD---TPQASRDVGLVWGAUGGTLVLLVLLAGGFL 369
 QY 386 GHYLRHKGTYLTHEAKSGDDADPADTALINAEGCGSGDDKKEYF 431
 Db 370 ALLILRRRRRKSPGGGND-----GDRGSYDPKTVQV 402

RESULT 7
 JC5287
 SHP subtrate-1 protein - human
 C/Species: Homo sapiens (man)
 C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
 C/Accession: JC5287
 R/Yamao, T.; Matsuoka, K.; Matsuoka, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
 Biochem. Biophys. Res. Commun. 231, 61-67, 1997
 A/Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
 A/Reference number: JC5287; MUID:97223399; PMID:9070220
 A/Contents: Brain
 A/Accession: JC5287
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-503 <YAM>
 A/Cross-references: DDBJ:D86403; MID:g1864010; PID:BAAL2974.1; PID:g1864011
 C/Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
 acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
 C/Genetics:
 A/Map position: 20p13

Query Match 10.5%; Score 238.5; DB 2; Length 503;
 Best Local Similarity 24.2%; Pred. No. 2.3e-09;
 Matches 110; Conservative 71; Mismatches 152; Indels 121; Gaps 23;
 QY 8 LLLLLLFPACWAPGGANLSQDGWQFODLELGTAPLDEALISTVWSSPDMLASQDSQP 67
 Db 14 LLCLLLAASCANS-----GVAGEELQV--IQP-DKSVS----- 44
 QY 68 WTSDETVAAGTVLKGQVXKHEDSSL-----QW-----SNPAQOTLYFGKRALDRNIQ 118
 Db 45 -----VAAGESAILHCTV-----TSLIPVGPQIOWFRGAGPARELIY-NQKEGHFPRVIT 92
 QY 119 LVITSTPE---LSSISNVALADGEVTCSTFTMPVETAKSLVTLVGIPOKPII 169
 Db 93 VSESTKRENMDFSISITNIPADAGTYCYVKFRKSGPDTEFKSGAGTSLSVRAKPSAPVV 152
 QY 170 TGYKSSUREKDTATLNCOSGSKFA-ARLTWRKQDLHGEPTRIQEDPNGK--TFTVSS 226
 Db 153 SGFAARATPQHTVSFCESHGFRDITLAKFNGNELSDQFNV--DPVGESVSYSIHS 210
 QY 227 SVTFQVTRDDGASIVCSVNHESLKGAD-RSTSQRIEVLVPTTAMIRPDPHPREGOKLL 285
 Db 211 TAKWLTREDVHSGVCEVAHVTLQGDPLRGATNLSETIRVPTLEVTQQPVRAENQ-VN 269

QY 286 LHCEGRG-NPVPQOYLWEKESVPLKMTQESALIFPLNKSDSGTYGCTATNSMGSKA 344
 Db 270 VTQVRKFYQRLQLTWLENGV---SRTEASTV---TENKDGTY-----NWMS 313
 QY 345 YYTLNV-----NDPSPVPS-----SSSTVHAIIG-----I 370
 Db 314 WLLVNVSAHRDDVKLTQCVHEHDQPAVSKSHDLKVSAPKPEQGSNTAAENTGSNERIYI 373
 QY 371 VAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGS 404
 Db 374 VGVWCTLLVALLMAALYLVRIR---OKKAQGS 403

RESULT 8
 I68093
 PRR2 delta - human
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C/Accession: I68093
 R/Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
 Gene 159, 267-272, 1995
 A/Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
 A/Reference number: I53960; MUID:95347610; PMID:7622062
 A/Accession: I68093
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-538 <RES>
 A/Cross-references: GB:S79172; NID:g1042204; PID:g1042205
 C/Genetics:
 A/Gene: PRR2delta
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.0%; Score 225.5; DB 2; Length 538;
 Best Local Similarity 23.9%; Pred. No. 2.1e-08;
 Matches 82; Conservative 52; Mismatches 146; Indels 63; Gaps 13;
 QY 77 GGTWVLKCOV-----KQED-----SSLOWSNPAQOTLYP- 106
 Db 47 GGTVELPCHLLPVPGLYISLTWQRPDAPANHONVAAPHKMGSPFPSPKGSERLSFV 106
 QY 107 -GEKRALDRNIQLVSTSTHELSSISNVALADGEVTCSTFTMPVETAKSLVTLVGIPO 165
 Db 107 SAKQSTGQTEAELODAT-----LALHGLTVEDEGNTCEFATFPKGSVRGM-TWLRVIA 160
 QY 166 KP---IITGYKSSUREKDTATLNCOSGSKFAARLTWRKQDLHGEPTRIQEDPNGKTF 223
 Db 161 KPNQQAQKVTFSPQPTTVALCISKEGPPARISW-LSSLDWEAKETQVSGTLG-TVT 218
 QY 224 VSSSVTFQVTRDDGASIVCSVNHESLKGADRSSTORIEVLVPTTAMI-----RP 273
 Db 219 VTSRFTLVPSGRADGVTVTKVEHSFE-EPALIPVTLVSRVTPPEVSIISGYDDNWYLGRT 277
 QY 274 DPHPREGOKLLHCEGRGNPVPQOYLWE-KEGSVPPLKMTQESALIFPLNKSDSGTYG 332
 Db 278 D-----ATLSCDVRNSNPETGYDWTSTGTPSTSAVAGSQSLVIAHVDLSLFTTFV 328
 QY 333 CSTATNSMGSKAYITLVNDPSPVPSSSTYHAIIGGIVAFIV 375
 Db 329 CVTVNAVGMGRAEQVIFVRE-TPTNAGATGATGGIIGGIIAII 370

RESULT 9
 JC5519
 50K Glycoprotein precursor - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Nov-2000
 C/Accession: JC5519
 R/Hancock, K.A.; Gooley, A.A.; Jeffrey, P.L.
 Mol. Brain Res. 44, 273-285, 1997
 A/Title: AvGP50, a predominantly axonally expressed glycoprotein, is a member of the Igi
 A/Reference number: JC5519; MUID:97225899; PMID:9073169
 A/Accession: JC5519

A:Molecule type: mRNA
A:Residues: 1-66, A', 68-417 <MEN>
A:CROSS-references: GB:M29535
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C:Genetics:
A:Gene: GDB:PVR; PVS
A:CROSS-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F:21-343/Domain: extracellular #status predicted <EXT>
F:21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>
F:42-125/Domain: immunoglobulin homology <IMW1>
F:159-223/Domain: immunoglobulin homology <IMW2>
F:259-314/Domain: immunoglobulin homology <IMW3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-417/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 11.7%; Score 265; DB 1; Length 417;
Best Local Similarity 26.6%; Pred. No. 2.4e-11;
Matches 106; Conservative 59; Mismatches 173; Indels 62; Gaps 17;

QY 5 AASLLLLLLFACCAWPGGANLSQDGYWQBDLELTP--LDEAISSTVW--SSPDMLA 61
DB 7 AAWPLLLVALLVSWPPPGTG-----DVVQAPQTQVPGFGLGDSVTLPYLOVPMNEV 58
QY 62 SQDSQ--PWSDETVAGTVVLKQVKDHEDSSLOWNSPAQQTLYPGEKRALRDNRQLV 120
DB 59 THVSQLTWT-----RHGSGSMVAFHQTQGPSYSEK-----RLEFV 95
QY 121 TSPHELSSISNVAL-----ADSGEYTCSTFTMPVTRAKSLVTLVGLPQKPIITG-- 171
DB 96 AA-----FLGELNRLNARLMPGLRVEDSGNYTCLPVTFF--QGSRSVDLWLRAPQNTAEV 151
QY 172 YKSLREKDTATLNCQSSGKPAARLTWRKGDQELHGEPTRIQEDPN--GKFTVSSSVT 229
DB 152 QKVLTGEPVPMARCVSTGRPPAQITWH--SDLGMPNTSQV--PGFLSGTIVTISLWT 207
QY 230 FQWTRDDGASIVCSVNHSLKADGSTQRIEVLVTPAMIRPDPPHREGO--KLLHLC 288
DB 208 LVPSSQVDGKNTCKVEHSEFEPKQLLT--VNLTVYYPPEVSGYDNNWYLGQNEATLTC 266
QY 289 EGRGNFVPOQYLWEKE--GSVPPPLKMTQESALIPFLNKSQDGYGCTATSNMGSYKAYT 347
DB 267 DARSNPEPTGYNWSVTMGPLPFAVAQAGQLLRPVDKPIINTLNCVNLGARGOAEIT 326
QY 348 LNVNDSPVSSSTVHAIGGIVAFIVFLLLMFLFLG 386
DB 327 VQVKEGPPSEHSGMSRNAII-----FLVLGILVFLILG 360

RESULT 5
AS3437
poliovirus receptor mpvr - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
A:Reference number: A53437
A:Accession: A53437
R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with p
A:Reference number: A53437; MUID:94179228; PMID:8132569
A:Accession: A53437
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <AOX>
A:CROSS-references: GB:D26107; NID:9475017; PIDN:BAA05103.1; PID:9825507
A:Experimental source: C57/Bl6, brain
A>Note: sequence extracted from NCBI backbone (NCBI:146664, NCBI:146667)

C:Superfamily: poliovirus receptor; immunoglobulin homology
F:47-133/Domain: immunoglobulin homology <IMW>
Query Match 11.3%; Score 256; DB 2; Length 530;
Best Local Similarity 24.4%; Pred. No. 1.4e-10;
Matches 100; Conservative 52; Mismatches 160; Indels 98; Gaps 16;

QY 3 APAASLLLLLLFACCAWPGGANLSQDGYWQBDLEL-----GT-----LAP 44
DB 13 SPTPLPLPILLLL-----LQETG---AQDVRVRLPEVRGLGGTVLPCHLPP 59
QY 45 LDEAISSTVSSPDMLASQDSQFWSDETVAAGTVVLKQVKDHEDSSLOWNSPAQQT 104
DB 60 TTERVVSQVWORLD-----GTVV-----AAHFPSFGVDFPN----- 90
QY 105 YGKERALRDNRQLVTSPT-----HELSSISNVALADEGEYTCSTFTMPVTRAKSLV 158
DB 91 -----SQFSKDRLSFVRARPETNADLRDATLAFRLGRVDEGNYTCEFATFNGTRRG-V 144
QY 159 TVLGIPIQKP--IITGYKSSLREKDTATLNCQSSGKPAARLTWRKGDQELHGEPTRIQED 216
DB 145 TWLRVIAQEPENAEAEQEVITIGQSVAVARCVSTGRPPARITW-----ISSLGKAKDTQBP 201
QY 217 P--NGKFTVSSSVTQVTRDDGASIVCSVNHSLKADGSTSQRIEVLVTPAMIRPD 275
DB 202 GIQAGTVTIIISYSLVPVGRADGVKTCRVEHSEFEE-----PILLPVLSVRYPP 252
QY 276 PHREG-----QKLLHCEGRNVPVPOQYLNE--KEGSPVPLKMTQESALIFPFLNK 325
DB 253 EVSISGYDNNWYLGRLSEAILTCDVRNSPEPTDYDWSITTSVFPFAGAVAGSOLLVHSVDR 312
QY 326 SDSGTGYGCTATSNMGSYKAYTYTLNVNDPSPVSSSTVHAIGGIVAFIV 375
DB 313 MUNTFFICTATNAVGTGRABQVILVRE--SPTAGAGATGGIIGGIIAII 361

RESULT 6
HLMSP3
poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
A:Accession: A38211
R:Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A:Reference number: A38211; MUID:92219365; PMID:1560525
A:Accession: A38211
A:Molecule type: DNA
A:Residues: 1-467 <MOR>
A:CROSS-references: GB:M80206; NID:919785; PIDN:AAA39734.1; PID:9199786
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovirus receptor homolog #status predicted <EXT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:167-231/Domain: immunoglobulin homology <IMW1>
F:167-231/Domain: immunoglobulin homology <IMW2>
F:267-322/Domain: immunoglobulin homology <IMW3>
F:355-374/Domain: transmembrane #status predicted <TMN>
F:375-467/Domain: intracellular #status predicted <INT>
F:154-131,174-229,274-320/Disulfide bonds: #status predicted
F:128,136,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 254.5; DB 1; Length 467;
Best Local Similarity 23.2%; Pred. No. 1.5e-10;
Matches 108; Conservative 59; Mismatches 186; Indels 113; Gaps 17;

QY 3 APAASLLLLLLFACCAWPGGANLSQDGYWQBDLEL-----GT-----LAP 44
DB 13 SPTPLPLPILLLL-----LQETG---AQDVRVRLPEVRGLGGTVLPCHLPP 59
QY 45 LDEAISSTVSSPDMLASQDSQFWSDETVAAGTVVLKQVKDHEDSSLOWNSPAQQT 104

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 12.4885 Seconds
(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

Sequence: 1 MGAPASLLLLLLLLLACWA.....AIINAEQGSGGDDKKEYFI 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283365

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	12.0	417	2 A44194	poliovirus recepto
2	270.5	11.9	392	2 B44194	poliovirus recepto
3	265	11.7	392	1 RWHUPD	poliovirus recepto
4	265	11.7	417	1 RWHUPA	poliovirus recepto
5	256	11.3	530	2 A53437	poliovirus recepto
6	254.5	11.2	467	1 HLMPF3	poliovirus recepto
7	238.5	10.5	503	2 JCS287	SHP substrate-1 pr
8	225.5	10.0	538	2 I68093	PRR2 delta - human
9	223	9.8	338	2 JCS519	50K glycoprotein p
10	221.5	9.8	518	2 JC4024	poliovirus recepto
11	217	9.6	5175	2 T20992	hypothetical prote
12	217	9.6	5198	2 T43290	hemocentin precurs
13	216.5	9.6	702	2 A36319	cardiomyoblastic a
14	215	9.5	739	2 JS0675	vascular cell adhe
15	213.5	9.4	478	2 I53960	PRR2 alpha - human
16	212.5	9.4	583	2 I39428	alcam - human
17	209	9.2	4391	2 A38096	perlecan precursor
18	208	9.2	338	2 JCI238	opioid-binding pro
19	208	9.2	345	2 JCI239	opioid-binding pro
20	208	9.2	1612	2 J30805	dutt1 protein - mo
21	207	9.1	345	2 JC4025	opioid-binding cel
22	207	9.1	7962	2 I38346	elastic titin - hu
23	205	9.1	338	2 JC4776	limbic-system-asso
24	204	9.0	509	2 JCS288	SHP substrate-1 pr
25	204	9.0	513	2 JCS289	SHP substrate-1 pr
26	203	8.9	345	2 S03199	opioid-binding pro
27	202	8.9	1651	2 T14160	transmembrane rece
28	197.5	8.7	547	1 S28904	intercellular adhe
29	196	8.7	344	2 I56551	neurotrimin - rat

ALIGNMENTS

RESULT 1

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C/Species: Cercopithecus aethiops (green monkey, grivet)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C/Accession: A44194

R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A/Title: A second gene for the African green monkey poliovirus receptor that has no puta

A/Reference number: A44194; MUID:93059651; PMID:1331506

A/Accession: A44194

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-417 <XOI>

A/Cross-references: GB:S48777

C/Superfamily: poliovirus receptor; immunoglobulin homology

C/Keywords: transmembrane protein

F/259-314/Domain: immunoglobulin homology <IMM>

Query Match	12.0%;	Score	272;	DB	2;	Length	417;
Best Local Similarity	26.2%;	Pred. No.	7.5e-12;				
Matches	106;	Conservative	56;	Mismatches	183;	Indels	60;
Gaps	16;						
QY	67	PWTSDETVVA	-----GGTVVLKC--QVKHED---SSLOWNPAQ-----	QT	103		
Db	24	PGTGDIIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSLQTSRHHGSGSMAVPHQTG	83				
QY	104	LYFGEKRALRDNRQLQVLTSTPHELSSISNVALADGEYTCSTFTMPVRTAKSLVTVLGI	163				
Db	84	PNYSEPKRLEFVAARLGTGL-RLASLRMFGLRVEDGNTCLFVTTP-OGSRSVDIWLRL	141				
QY	164	PKQPIITG--YKSSIREKDTATINCQSSGSKPAARLTWRKQDLHGEPTRIQEDEN--G	219				
Db	142	LAKPONTAEVQVQLTGKVPVAVRCVSTGGRPPAHITWH---SDLGMENTQA-PGFLS	197				
QY	220	KFTFTSSSVTFQVTRDDCASIVCSVNHSLKAGDRSTSORIEVLYTPTAMIRP-DPPHP	278				
Db	198	GVTVTSLWILVPSSQVQDGKSVTCVHEHSEPKQLLT-VNLTVVYPPEVSISSGVNNWY	256				
QY	279	REGQKLLHCEGRGNVPQOYLWEKE-GSVPLKMTQESALIFPFINKSDSTYGTGTS	337				
Db	257	LSQNEATITCDARSNPETGYNNSTMTGPLPFVAQAQQLLIRVPDPIPTFTTCNVN	316				
QY	333	NMGSKAYTYTLNVND-PSFPVSSSTYHAIIGGIVAFVFLLLIMLIFLG-----	386				
Db	317	ALGAQAELTVQVKEGPPSEFGMS-----NIIFLLIGVILLTLIGVGYRRC	370				
QY	387	-----HYLRHKGTYYLTHAKGSDDPADPATINAEQGSGG	424				
Db	371	SREFLWCHHLSFSSBEHASAGANGYISYSDVSREASSQDPQTEG	415				

heparan sulfate pr
tumor suppressor -
kinase-like protei
neogenin - chicken
irregular chiasm C
hypothetical prote
hypothetical prote
neuroilin - goldfis
adhesion molecule
surface glycoprote
connectin/titin -
sax-3 protein - Ca
probable advanced
colon carcinoma-as
lutheran blood gro
neuromusculin - fr


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RESULT 12
US-09-905-125A-84
; Sequence 84, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

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; APPLICANT:      Baum, Peter
; TITLE OF INVENTION:      Molecules Designated B71L1
; FILE REFERENCE:      2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER:      PCT/US99/17906
; PRIOR FILING DATE:      1999-08-05
; PRIOR APPLICATION NUMBER:      60/095,563
; PRIOR FILING DATE:      1998-08-07
; NUMBER OF SEQ ID NOS:      22
; SOFTWARE:      PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

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Query Match	33.3%;	Score	732.5;	DB	4;	Length	398;
Best Local Similarity	38.3%;	Pred. No.	6.5e-57;				
Matches	162;	Conservative	74;	Mismatches	144;	Indels	43;
						Gaps	8;

QY	10	LLLLLSAAALIPGT-----DGQMLFTKDVITIEGEVATISCVQNKSDSDSVIQLLNPNRQ	64
Db	9	LLLLLLFACCAWAGGAMLSDQDPQTSDETVVAGGTIVLKQVKDHEDSLQSNPAQQ	68
QY	65	TVYFRDPRPKDRFQLNFSSELKSVLINVSIISDEGRYFCOLYTOPPOESYTTITVLV	128
Db	69	TLYFGEKRALDRNRIQLVTSPTHELSSISNVALADEGYTCSIFTMPVRTAKSLVTVLG	128
QY	125	PPRLMLIDIOKDTAVEGEEIEVNCTANASKEATTIRWFKNGKELKGK-SEVEEWSDD--MY	181
Db	129	IPOKPIITGYKSLREKDTATLNCQSGSGSPAARLTWKQGBQELHGEPTTRIQEDPNKGT	188
QY	182	TVTSQMLMLKVHKEDDGVPIVCQVEHPAVTG-NLQTRYLEVYQVKPQVHIQMTVPLOQLTR	240
Db	189	TVSSSVTFQTRDDDGASIVCSVNHESLKGADRSITSQRIEVLVYTPTAWIIPDDP--HPR	245
QY	241	EGDAFELTCEAIKGPQPMVTVTVVDDEMQHVLSPNLI FINNLKTDNGTVYRCEASNI	300
Db	246	EQQKLLHCEGRGNPVPQOVLWEK-EGSVPLPKMTQESALIFPFLNKSDDSGTYGCTATSN	304
QY	301	VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTLTITDTSRAGEGTIGAVDHA	360
Db	305	MGSKYKAYTLNVNDPS---PVPSSSTY-----HAIIG	334
QY	361	GVYAVVVEAMLCLLIILGRYFARKGTYFTTHEAKGADDAADATATINAGGQNNSEKK	420
Db	335	GIYAFIVFLLMLIIFLGHYLI RHKGTYLTHEAKGSDDPADPADTAINAEGGSGGDDK	394
QY	421	EYF	423
Db	395	EYF	397

RESULT 11
US - 907-79A-84
/ Sequence 84, Application US/0907794A
/ Patent No. 6635468
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-84

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Query Match	33.3%;	Score 732.5;	DB 4;	Length 398;
Best Local Similarity	38.3%;	Pred. No. 6.5e-57;		
Matches 162;	Conservative	74;	Mismatches 144;	Indels 43; Gaps 8
QY	10	LLLLLSAALIFTG-----DGNLFKDVTVIEGEVATIS	CCQVNSKDDSVIQLLNPRQ	64
Db	9	LLLLLFACWAPGGANLSODDSQPTWSDTVVAGGTWVLK	CCQVKYHEDSLSOWNSPAQQ	68
QY	65	TIYFRDPRPKOSRFOLLNPFSSSELKSVLTNVSISDEGR	YFCOLYTDPPQBSYTTITVLV	124
Db	69	TLYFGEKRALRDNRILQVLTSTPHELSISISNVALADEG	YTCSTFTMPVTKSLVTVLG	128
QY	125	PPRLMIDTQKQTAVGEESIEVNCNTAMASKPATTIRWF	KKNELKLGK-SEVEEWSD--MY	181
Db	129	IPQKPIYTKSRLREKFDATLNCQSSGSPFAARLTWRKGD	OEHLHGPTPTIOEDPNGKTF	188

Db 363 VVFTLCSIFLLGRYLARHKGTYLTNEAKGADPADADTAIINAEAGSQVNAEKKKEYF 420

RESULT 8
US-08-660-531-1
; Sequence 1, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-660-531-1

Query Match 40.7%; Score 893.5; DB 3; Length 421;
Best Local Similarity 45.0%; Pred. No. 3.3e-71;
Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

QY 26 GQNLFTKDVTVIEGEVATISQVNSKSDSVIQLNPNRQTYFRDPRPLKDSRFQLLNFS 85
Db 10 GQFLPTQNVTVVEGGTALITCRDQNTSLQSNPAQQTLYFDKALRDNRIELVRAS 69

QY 86 SSELKVSILNVSIDEGRYFCOLYDPPQESYTTITVLVPPNLMIDIQKOTAVEGEIE 145
Db 70 WHELISIVSDVSLDEGQTCSLFTMPVKTSKAYLTVLGVPEKQPSGFSPPVMEGLMQ 129

QY 146 VNCTAMAKPATIRFWKGNKELKGKSEVEWS---DMYTVTSQMLKVHKEDDGVVIC 202
Db 130 LTKCTSGSKFAADIRWKNDEIKDKVYLKEDANRKTFTVSTLDFRVRSDDDGVVIC 189

QY 203 QVEHPAVTGNLQ--TORYLEVQKYPQVHIQMTYPLQGLTREGDAFELTCEAIKGPQVMT 261
Db 190 RVDHESINATQVAMQVLEIHYTPSVKI---IPSTFPQEGQPLILTCESKGPPEPUL 246

QY 262 WVRVDEM--PQHVLSPNLFINNKNKTNGTYRCEASNIVGKAHSDYMLYVYDPPPTI 319
Db 247 WTKDGGELPDDPRWVVSRELNILFNKNTDNGTYRCEATNTIGSSASBYVLIVDHPNTL 306

QY 320 PPPTTTTTTTTTTTTTTTTT-----DSRAGEGTIGAVDHAVIGGVAV 365
Db 307 LPTTIIPSLTATVTTTVAITTSPTTSATTSIRDPNALAGNGP----DHALIGGIVAV 362

QY 366 VVFAMCLLIILGRYFARHKGTYTHEAKGADDAADADTAIINAEAGSQVNAEKKKEYF 423
Db 363 VVFTLCSIFLLGRYLARHKGTYLTNEAKGADPADADTAIINAEAGSQVNAEKKKEYF 420

RESULT 9
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B711
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PPT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match 33.6%; Score 738.5; DB 4; Length 398;
Best Local Similarity 38.8%; Pred. No. 1.9e-57;
Matches 165; Conservative 73; Mismatches 136; Indels 51; Gaps 9;

QY 12 LLLLSAAALIPTG-----DQNLFTKDVTVIEGEVATISQVNSKSDSVIQLNPNRQTI 66
Db 11 LLLLLACSWAPGGANLSQDSSQPTWSTDEIVAGTVLKCQVKDHDSSIQWNSNPAQQTLL 70

QY 67 YFRDPRPLKDSRFQLLNFSSELKVSILNVSIDEGRYFCOLYDPPQESYTTITVLVPP 126
Db 71 YFGEKRALRDNRIOLVSTSPHLSISINVALADEGEYTCSTFTMPVTKSLVTVLGP 130

QY 127 RNLMDIQKDTAVEGEEIEVNCVTAMASKPATIRFWKGNKELKG--KSEVEWSD--MYTV 183
Db 131 QKPIITGYKSSLREKETATINLCQSSGSKPAAOLTWRKQDQLHGDQTRIQEDPNGKTFV 190

QY 184 TSQMLKVHKEDDGVVICQVEHPAVTG--NLQORYLEVQYKYPQVHIQMTYPLQGLTREG 242
Db 191 SSSVSFQVTRDGDGANIVCSVNHESILKGADRSQSRIEVLVYPTAMIR---PEPAHPREG 247

QY 243 DAFELTCEAIKGPQVMTVWVVDDEMP-----QHAVLSGPNLFINNKNKTNGTYRCEAS 298
Db 243 QKLLHCSGRGNPVPQVYVWVKEGSEPELKMTOESALIFP-----FLNKSDSGTGTCTAT 302

QY 299 NIVGKAHSDYMLYVYDPPPTTTPPTTTTTTTTTTTTTTTTTTTTTITLITDSRAGEGTIGAVDHAV 358
Db 303 SNMGSYTAVFTLVNDPS---PVSSSSSTY-----HAI 332

QY 359 IGVVAVVVFAMCLLIILGRYFARHKGTYTHEAKGADDAADADTAIINAEAGSQVNAEKKKEYF 418
Db 333 IGGIVAFIVFVLLILLIFLGHYLRHKGTYLTHEAKGSDPADADTAIINAEAGSQVNAEKKKEYF 392

QY 419 KKEYF 423
Db 393 KKEYF 397

RESULT 10
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:


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; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-531-5

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Query Match      41.1%; Score 904; DB 3; Length 444;
Best Local Similarity 44.7%; Pred. No. 4.2e-72;
Matches 194; Conservative 74; Mismatches 136; Indels 30; Gaps 7;

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QY 13 LLSAAA---LIPGDKQLFKDVTVEGEVATISQVKNKSDSVIQLLNPNQTIYFR 69
DB 17 LLLQAASKNKVKSGQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQWNPAAQQTLYFD 76
QY 70 DFPLKDSRQLNFSSELKVLSTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPNRL 129
DB 77 DKKALDRNRIELVRASWHELSSVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKP 136
QY 130 MIDIQKTAVEGEIEVNCCTAMASKPATTIRWFGKNEKLGKSEVEWS---DMYVTTSQ 186
DB 137 QISGSPVMEGLMQLTCTSGSKPAADIRWFKNDKEIKDVLYLKBEDANRKTFTVSST 196
QY 187 LMLKVKHEDDGPVICOVEHPAVTGNLQ--TORYLEVQYKQVHIQMTYPLQGLTRGDFA 245
DB 197 LDFRDRSDGVAICRVDSHESLNATPQVAMQVLEIHYTPSVKI---IPSTPPQGGQPL 253
QY 246 ELTCEALGKQPQVMTWVRVDDM--POHAVLSGPNLFNNLNKTDNGTYRCEASNIVGK 303
DB 254 ILTCEGKGLPEPLVMTKDGGLPDPDRMVVSGRELNLFNKTNDNGTYRCEATNIQ 313
QY 304 AHSYDMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 423
DB 314 SSAEYVLIVHDVNTLLPTTIIISLTATVTTTVAITTSPTTSATTSIRDPNALAQNG 373
QY 350 TIGAVDHAVIGGVAVVVFAMLCIIILGRYFAHKGTYTTHAKGADDAADATAIINA 409
DB 374 P-----DHALIGGVAVVVFVFLCSIFLLGRYLARHGKTYLTHAKGAEDAPADTAIINA 429
QY 410 EGGQNNSEKKEYF 423
DB 430 EGSQVNAEKKKEYF 443

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RESULT 7
US-08-659-984A-1
; Sequence 1, Application US/08659984A

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; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-984A-1

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Query Match      40.7%; Score 893.5; DB 2; Length 421;
Best Local Similarity 45.0%; Pred. No. 3.3e-71;
Matches 188; Conservative 73; Mismatches 130; Indels 27; Gaps 6;

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QY 26 GQNLFKDVTVEGEVATISQVKNKSDSVIQLLNPNQTIYFRDPRPKDSRQLNFS 85
DB 10 GQFPLTQNTVVEGGTALTCTCRVDQNDNTSLQWNPAAQQTLYFDKKALDRNRIELVRAS 69
QY 86 SSELKVLSTNVSISDEGRYFCOLYTDPPQESYTTITVLVPPNLMIDIQKTAVEGEIE 145
DB 70 WHELSSVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFSFVMEGLMQ 129
QY 146 VNCTAMASKPATTIRWFGKNEKLGKSEVEWS---DMYVTTSQMLKVKHEDDGPVTC 202
DB 130 LTCKTSGSKPAADIRWFKNDKEIKDVLYLKBEDANRKTFTVSSTLDFRDRSDGVAIC 189
QY 203 QVEHPAVTGNLQ--TORYLEVQYKQVHIQMTYPLQGLTRGDFAFELTCEALGKQPQVMT 261
DB 190 RVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPPQGGQPLLTCEGKGLPEPL 246
QY 262 WVRVDDM--POHAVLSGPNLFNNLNKTDNGTYRCEASNIVGKASHSYMLVYDPTTI 319
DB 247 WTKDGGELPDPDRMVVSGRELNLFNKTNDNGTYRCEATNIQSSAEYVLIVHDVNTL 306
QY 320 PPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 365
DB 307 LPTTIPLSTTATVTTTVAITTSPTTSATTSIRDPNALAQNGP-----DHALIGGVAV 362
QY 366 VVFAMLCIIILGRYFAHKGTYTTHAKGADDAADATAIINAFGGQNNSEKKEYF 423

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GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretasins
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend

QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADAADTAIINAEGGONNSEKK 420
Db |||||
QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADAADTAIINAEGGONNSEKK 420
Db |||||
QY 421 EYF 423
Db |||||
QY 421 EYF 423

RESULT 2

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

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Best Local Similarity 98.8%; Pred. No. 1.2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLSAAALIPGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
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Db 79 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSITNVSISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPRLNLMIDIKQDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPRLNLMIDIKQDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 258
QY 241 EGDAFELTCEAIGKPOPMVMTVRVDDMPQHAVLSGPNLFINNKNKTNGTYRCEASNI 300
Db 259 EGDAFELTCEAIGKPOPMVMTVRVDDMPQHAVLSGPNLFINNKNKTNGTYRCEASNI 318
QY 301 VGKASHDMLYVYDPTTTPPTTT 360
Db 319 VGKASHDMLYVYDPTTTPPTTT 378
QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADAADTAIINAEGGONNSEKK 420
Db 379 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADAADTAIINAEGGONNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 3

US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 98.7%; Score 2169; DB 4; Length 442;
Best Local Similarity 98.8%; Pred. No. 1.2e-184;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLSAAALIPGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
Db 19 AAPGLRLRLLLLSAAALIPGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSITNVSISDEGRYFCQLYTDPPQESYTTI 120
Db 79 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSITNVSISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPRLNLMIDIKQDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPRLNLMIDIKQDTAVEGEEIEVNCTAMASKPATIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQRYLEYVQKPOVHIQMTYPLQGLTR 258
QY 241 EGDAFELTCEAIGKPOPMVMTVRVDDMPQHAVLSGPNLFINNKNKTNGTYRCEASNI 300
Db 259 EGDAFELTCEAIGKPOPMVMTVRVDDMPQHAVLSGPNLFINNKNKTNGTYRCEASNI 318
QY 301 VGKASHDMLYVYDPTTTPPTTT 360
Db 319 VGKASHDMLYVYDPTTTPPTTT 378
QY 361 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADAADTAIINAEGGONNSEKK 420
Db 379 GVVAVVVFAMLCIIILGRYFARHKGTYFTHKAGDADAADTAIINAEGGONNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 4

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 15.4726 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-4
Perfect score: 2197
Sequence: 1 AAPPGLRLRLLLLSAAL.....TAINAEGQNNSEKKEYF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B COMB.pcp.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*
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6: /cgn2_6/prodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	423	4	US-09-778-510-22
2	2169	98.7	442	4	US-09-778-510-20
3	2169	98.7	442	4	US-09-930-803-1
4	2149	97.8	440	4	US-09-866-028-61
5	904	41.1	444	2	US-08-659-984A-5
6	904	41.1	444	3	US-08-660-531-5
7	893.5	40.7	421	2	US-08-659-984A-1
8	893.5	40.7	421	3	US-08-660-531-1
9	738.5	33.6	398	4	US-09-778-510-4
10	732.5	33.3	398	4	US-09-907-794A-84
11	732.5	33.3	398	4	US-09-778-510-6
12	732.5	33.3	398	4	US-09-905-125A-84
13	732.5	33.3	398	4	US-09-902-775A-84
14	715.5	32.6	432	4	US-09-778-510-2
15	333	15.2	227	4	US-09-205-258-947
16	252.5	11.5	517	4	US-09-723-368-4
17	244	11.1	518	4	US-09-919-172-20
18	231.5	10.5	393	1	US-08-429-742-2
19	226.5	10.3	479	4	US-09-723-368-2
20	220.5	10.0	344	4	US-09-700-397-3
21	216	9.8	458	4	US-09-435-956A-1
22	212	9.6	313	4	US-09-700-397-4
23	206.5	9.4	308	2	US-08-414-657D-46
24	206.5	9.4	325	2	US-08-414-657D-2
25	206.5	9.4	325	2	US-08-414-657D-41
26	206.5	9.4	325	4	US-09-135-080-2
27	206.5	9.4	338	4	US-09-976-594-404

28	206	9.4	388	1	US-08-429-742-4	Sequence 4, Appli
29	205.5	9.4	582	4	US-09-702-705-334	Sequence 334, App
30	205.5	9.4	582	4	US-09-736-457-334	Sequence 334, App
31	205.5	9.4	582	4	US-09-614-124B-334	Sequence 334, App
32	205.5	9.4	582	4	US-09-671-325-334	Sequence 334, App
33	205.5	9.4	582	4	US-09-589-184-334	Sequence 334, App
34	204.5	9.3	315	2	US-08-414-657D-47	Sequence 47, Appl
35	204.5	9.3	338	2	US-08-414-657D-42	Sequence 42, Appl
36	204.5	9.3	338	4	US-08-414-657D-43	Sequence 43, Appl
37	204.5	9.3	338	4	US-09-135-080-4	Sequence 4, Appli
38	204	9.3	642	1	US-08-217-299-1	Sequence 1, Appli
39	204	9.3	698	2	US-08-602-725-36	Sequence 36, Appl
40	204	9.3	734	3	US-08-389-459A-17	Sequence 17, Appl
41	204	9.3	734	3	US-08-987-867A-17	Sequence 17, Appl
42	203.5	9.3	583	2	US-08-432-016-2	Sequence 2, Appli
43	203.5	9.3	583	2	US-08-684-594-2	Sequence 531, App
44	203	9.2	1461	4	US-09-976-594-531	Sequence 60, Appl
45	198.5	9.0	338	2	US-08-414-657D-60	

ALIGNMENTS

RESULT 1
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated BYL1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRI
; ORGANISM: Mus musculus
US-09-778-510-22

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Gaps		0						
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DB	1	AAPPGLRLRLLLLSAAL	1	FTGDGQNLFTKDVTVIEGEVATIS	COVNKSDSVIQLLN	60		
QY	61	PNRQIYFRDFRPLKDSR	61	PNRQIYFRDFRPLKDSR	PNRQIYFRDFRPLKDSR	120		
DB	61	PNRQIYFRDFRPLKDSR	61	PNRQIYFRDFRPLKDSR	PNRQIYFRDFRPLKDSR	120		
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DB	121	TVLVPRLMLDIOKDTAVE	121	TVLVPRLMLDIOKDTAVE	TVLVPRLMLDIOKDTAVE	180		
QY	181	YTVTSQLMLVKHEDDGP	181	YTVTSQLMLVKHEDDGP	YTVTSQLMLVKHEDDGP	240		
DB	181	YTVTSQLMLVKHEDDGP	181	YTVTSQLMLVKHEDDGP	YTVTSQLMLVKHEDDGP	240		
QY	241	EGDAFELTCEAIGKQP	241	EGDAFELTCEAIGKQP	EGDAFELTCEAIGKQP	300		
DB	241	EGDAFELTCEAIGKQP	241	EGDAFELTCEAIGKQP	EGDAFELTCEAIGKQP	300		
QY	301	VGAHSDYMLVYDPEPT	301	VGAHSDYMLVYDPEPT	VGAHSDYMLVYDPEPT	360		
DB	301	VGAHSDYMLVYDPEPT	301	VGAHSDYMLVYDPEPT	VGAHSDYMLVYDPEPT	360		

Db 377 GVVAVVFPAMLCLLIILGRYFARHKGTFTHEAKGADDAADADTAIINAEGGQNNSEKK 436
QY 421 EYF 423
Db 437 EYF 439

Search completed: May 27, 2004, 09:31:23
Job time : 49.4142 secs

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QY 197 YTVTSQMLKVHKEDDGVPIQVVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTR 256
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Db |||||
QY 257 EGDALFELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 316
QY 301 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db |||||
QY 317 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 376
QY 361 GVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEQGNNSSEKK 420
Db |||||
QY 377 GVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEQGNNSSEKK 436
QY 421 EYF 423
Db |||||
QY 437 EYF 439

RESULT 15
AAB01321
ID AAB01321 standard; protein; 440 AA.
XX
AC AAB01321;
XX
DT 25-SEP-2000 (first entry)
XX
DE Human PRO355 polypeptide.
XX
KW PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
KW PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353;
KW PRO361; transmembrane polypeptide; antibody; screening;
KW detection; inhibition; probe; primer; human.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide
FT 1. .36 Location/Qualifiers
FT /label= Signal peptide
FT Modified-site 9. .15 /note= "N-myristoylation site"
FT Modified-site 65. .69 /note= "N-glycosylation site"
FT Modified-site 99. .103 /note= "N-glycosylation site"
FT Modified-site 111. .115 /note= "N-glycosylation site"
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FT Modified-site 227. .233 /note= "N-glycosylation site"
FT Modified-site 233. .240 /note= "N-myristoylation site"
FT Modified-site 302. .306 /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 306. .310 /note= "N-glycosylation site"
FT Modified-site 307. .313 /note= "N-glycosylation site"
FT Modified-site 319. .328 /note= "N-myristoylation site"
FT Modified-site 365. .371 /note= "Tyrosine kinase phosphorylation site"
FT Domain /note= "N-myristoylation site"
FT /label= Transmembrane domain
FT Modified-site 372. .393 /note= "N-myristoylation site"
FT Modified-site 376. .382 /note= "N-glycosylation site"
FT Modified-site 402. .408 /note= "N-glycosylation site"
FT Modified-site 411. .417 /note= "N-glycosylation site"
FT Modified-site /note= "N-myristoylation site"

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FT Modified-site 427. .433 /note= "N-myristoylation site"
FT Modified-site 428. .432 /note= "N-myristoylation site"
FT Modified-site 430. .434 /note= "N-glycosylation site"
XX
FN WO200032776-A2.
XX
PD 08-JUN-2000.
XX
PF 01-DEC-1999; 99WO-US028301.
XX
PR 01-DEC-1998; 98WO-US025108.
XX
PR 16-DEC-1998; 98US-0112850P.
XX
PR 22-DEC-1998; 98US-0113296P.
XX
FA (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
PI Hillan KJ, Kljavin IU, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2000-412324/35.
DR N-PSDB; AAA49563.
XX
PT New human nucleic acids encoding secreted and transmembrane polypeptides,
PT designated as PRO polypeptides, useful as pharmaceutical and diagnostic
PT agents.
XX
PS Claim 12; Fig 24; 187pp; English.
XX
CC New human nucleic acids encoding secreted and transmembrane polypeptides
CC which are designated as PRO polypeptides are described The membrane-bound
CC proteins have various industrial applications, including as
CC pharmaceutical and diagnostic agents. The membrane-bound proteins can
CC also be employed for screening of potential peptide or small molecule
CC inhibitors of the relevant receptor/ligand interaction. Anti-PRO
CC antibodies are useful for the affinity purification of PRO from
CC recombinant cell culture or natural sources
XX
SQ Sequence 440 AA;
Query Match 97.8%; Score 2149; DB 3; Length 440;
Best Local Similarity 98.3%; Pred No. 5.8e-148;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
QY 1 AAPGRLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLN 60
Db 19 AAPPG--LRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLN 76
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Db 77 PNQTIYFRDPRPLKDSRFOLLNFSSELKYSLTNVSISDEGRYFCQLYTPDPQSYTTI 136
QY 121 TVLVPPRLNLMIDIQKTAVEGEETVNCVTAMASKPATIRFKGNKELKGKSEVEWSDM 180
Db 137 TVLVPPRLNLMIDIQKTAVEGEETVNCVTAMASKPATIRFKGNKELKGKSEVEWSDM 196
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Db 197 YTVTSQMLKVHKEDDGVPIQVVEHPAVTGNLTQRYLEVQYKQVHIQMTYPLQGLTR 256
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Db 257 EGDALFELTCEAIGKQPQVMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 316
QY 301 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 317 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 376
QY 361 GVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEQGNNSSEKK 420

```

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying a pain and a
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 442 AA;

XX Query Match 98.6%; Score 2166; DB 7; Length 442;

XX Best Local Similarity 98.6%; Pred. No. 3.4e-149;

XX Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVNSKSDSVIQLLN 60
Db 19 AAPGGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVNSKSDSVIQLLN 78
QY 61 PNRQTIYFRDFRPLKDSRFOLLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPQESYTTI 120
Db 79 PNRQTIYFRDFRPLKDSRFOLLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPQESYTTI 138
QY 121 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 180
Db 139 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 198
QY 181 YTVTSQMLKVKHEDGVPVICOVEHPAVTGNLQYKYLEVQKPVQVHQMTPLOGLTR 240
Db 199 YTVTSQMLKVKHEDGVPVICOVEHPAVTGNLQYKYLEVQKPVQVHQMTPLOGLTR 258
QY 241 EGDFAELTCEATGKPOVMVTVRVDDEMPQAVLSGPNLFNNLKNKTNGYRCEASNI 300
Db 259 EGDFAELTCEATGKPOVMVTVRVDDEMPQAVLSGPNLFNNLKNKTNGYRCEASNI 318
QY 301 VGKAHSDYMLYVDPPTTTPPTTT 360
Db 319 VGKAHSDYMLYVDPPTTTPPTTT 378
QY 361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHAKGADDAADADATIAAEGGQNNSEKK 420
Db 379 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHAKGADDAADADATIAAEGGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 14
AAV17830

ID AAV17830 standard; protein; 440 AA.
XX AC AAV17830;
XX DT 12-AUG-1999 (first entry)
XX DE Human PRO355 protein sequence.
XX KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
XX KW secreted protein; transmembrane protein; inflammation disorder.
XX OS Homo sapiens.
XX PN WO9928462-A2.
XX PD 10-JUN-1999.
XX PF 01-DEC-1998; 98WO-US025108.
XX PR 03-DEC-1997; 97US-0067411P.
XX PR 11-DEC-1997; 97US-0069278P.
XX PR 11-DEC-1997; 97US-0069334P.
XX PR 12-DEC-1997; 97US-0069335P.
XX PR 16-DEC-1997; 97US-0069425P.
XX PR 16-DEC-1997; 97US-0069696P.
XX PR 16-DEC-1997; 97US-0069702P.
XX PR 17-DEC-1997; 97US-0069870P.
XX PR 17-DEC-1997; 97US-0069873P.
XX PR 18-DEC-1997; 97US-0068017P.
XX PR 03-JAN-1998; 98US-0070440P.
XX PR 09-FEB-1998; 98US-0074086P.
XX PR 09-FEB-1998; 98US-0074092P.
XX PR 25-FEB-1998; 98US-0075945P.
XX (GETH) GENENTECH INC.
XX PI Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
XX WPI; 1999-3711118/31.
XX DR N-PSDB; AAX80055.
XX Nucleic acids encoding PRO secreted and transmembrane proteins.
XX Claim 12; Fig 27; 123pp; English.
XX The present invention describes nucleic acids encoding PRO secreted and
XX transmembrane proteins used therapeutically. The PRO proteins have
XX cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
XX activity. The proteins and polynucleotides can be used in therapy,
XX identification of homologues, raising antibodies and design of probes and
XX primers. They can be used in a range of diseases related to proteins that
XX they have homology with, e.g. a PRO protein having homology to complement
XX proteins may be used in inflammatory responses
XX Sequence 440 AA;
Query Match 97.8%; Score 2149; DB 2; Length 440;
Best Local Similarity 98.3%; Pred. No. 5.8e-148;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
QY 1 AAPGGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVNSKSDSVIQLLN 60
Db 19 AAPPG--LRLLLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVNSKSDSVIQLLN 76
QY 61 PNRQTIYFRDFRPLKDSRFOLLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPQESYTTI 120
Db 77 PNRQTIYFRDFRPLKDSRFOLLNFSSELKVSLSLTVNSISDEGRYFCQLYTDPQESYTTI 136
QY 121 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 180
Db 137 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGSVEEWSDM 196

CC represents a human p53 pathway modifying protein

XX Sequence 442 AA;

Query Match 98.6%; Score 2166; DB 6; Length 442;

Best Local Similarity 98.6%; Pred. No. 3.4e-149;

Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLLLSAAALPTGQNLPTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 Db 19 AAPGLRLRLLLLLLSAAALPTGQNLPTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
 QY 61 PNRTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIDEGRYFCQLYTDPQESYTTI 120
 Db 79 PNRTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPPRLNLMIDIQDRTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 180
 Db 139 TVLVPPRLNLMIDIQDRTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 198
 QY 181 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
 Db 199 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
 QY 241 EGDALFELTCEAIGKPKQPVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
 Db 259 EGDALFELTCEAIGKPKQPVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 318
 QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHA 360
 Db 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHA 378
 QY 361 GVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADADTAIINAEAGGQNNSEKK 420
 Db 379 GVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADADTAIINAEAGGQNNSEKK 438
 QY 421 EYF 423
 Db 439 EYF 441

RESULT 11

ABO07231

ID ABO07231 standard; protein; 442 AA.

XX AC ABO07231;

XX DT 13-AUG-2003 (first entry)

XX DE Human p53 modifying protein, SEQ ID 191.

XX KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;

XX KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;

XX KW lung cancer; ovarian cancer; angiogenesis; cell cycle;

XX KW apoptotic disorder; cell proliferation disorder.

XX OS Homo sapiens.

XX PN WO200299122-A1.

XX PD 12-DEC-2002.

XX PF 03-JUN-2002; 2002WO-US017382.

XX PR 05-JUN-2001; 2001US-0296076P.

XX PR 10-OCT-2001; 2001US-0328605P.

XX PR 15-FEB-2002; 2002US-0357253P.

XX PA (EXEL-) EXELIXIS INC.

XX PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX DR WPI; 2003-156859/15.

DR N-PSDB; ACD13404.

XX Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 XX pathway in *Drosophila*.

PS Example 2; Page 557-559; 678pp; English.

XX The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human ortholog of genes that modify the p53 pathway in
 CC *Drosophila*) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence
 XX represents a human p53 pathway modifying protein

SQ Sequence 442 AA;

Query Match 98.6%; Score 2166; DB 6; Length 442;

Best Local Similarity 98.6%; Pred. No. 3.4e-149;

Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLLLSAAALPTGQNLPTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 Db 19 AAPGLRLRLLLLLLSAAALPTGQNLPTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
 QY 61 PNRTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIDEGRYFCQLYTDPQESYTTI 120
 Db 79 PNRTIYFRDPRPLKDSRFQNLNFSSELKVSILTNVSIDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPPRLNLMIDIQDRTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 180
 Db 139 TVLVPPRLNLMIDIQDRTAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEWSDM 198
 QY 181 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
 Db 199 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
 QY 241 EGDALFELTCEAIGKPKQPVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
 Db 259 EGDALFELTCEAIGKPKQPVMTWVRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 318
 QY 301 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHA 360
 Db 319 VGKASDYMLYVYDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHA 378
 QY 361 GVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADADTAIINAEAGGQNNSEKK 420
 Db 379 GVAVVVFAMLCILIIILGRYFARHKGTFTHEAKGADDAADADTAIINAEAGGQNNSEKK 438

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XX 10-JUL-2003.
PD 18-APR-2001; 2001US-00836353.
XX 28-OCT-1998; 98US-0105971P.
XX 27-OCT-1999; 99MO-US025031.
PR 19-APR-2000; 2000US-0198407P.
XX (NIJJ//) NI J.
FA (YOUN//) YOUNG P E.
FA (KENN//) KENNY J J.
FA (OLSE//) OLSEN H S.
PA (MOOR//) MOORE P A.
PA (WEIY//) WEI Y.
FA (GREE//) GREENE J M.
FA (RUBE//) RUBEN S M.
XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
PI Ruben SM;
XX WPI; 2004-020335/02.
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX Disclosure; SEQ ID NO 136; 380pp; English.
XX The invention relates to an isolated nucleic acid sequence, or its
CC allelic variant, a fragment of the cDNA sequence, or its fragment,
CC domain, epitope or species homologue. The nucleic acid is useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition e.g., cancer, liver disorders such as hepatitis or neural
CC disorders such as Alzheimer's disease. The present sequence represents
CC the amino acid sequence of a novel human secreted protein associated
CC protein.
XX SQ Sequence 442 AA;
XX Query Match 98.7%; Score 2169; DB 8; Length 442;
XX Best Local Similarity 98.8%; Pred. No. 2.1e-149;
XX Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLLLLSAALLIPGCGNLFTKQVTVIEGEVATISQVNVKSDSVIQLLN 60
DB 19 AAPPGLRLRLLLLSAALLIPGCGNLFTKQVTVIEGEVATISQVNVKSDSVIQLLN 78
QY 61 PNRQTIYFRDRLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESVTTI 120
DB 79 PNRQTIYFRDRLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESVTTI 138
QY 121 TVLVPRLNLMIDIKQTAVERGEIEVNCCTAMASKPATTIRFWKGNKELKGSVEEWSDM 180
DB 139 TVLVPRLNLMIDIKQTAVERGEIEVNCCTAMASKPATTIRFWKGNKELKGSVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDQVPVICQVEHPAVTGNLTQRYLEVQKPVQHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDQVPVICQVEHPAVTGNLTQRYLEVQKPVQHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKQPFQVWVTVRVDDEMPQHAVLSGPNLFINLNKNTDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKQPFQVWVTVRVDDEMPQHAVLSGPNLFINLNKNTDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 360
DB 319 VGKASDYMLYVYDPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTPPTTTP 378
QY 361 GVAVVVVVFAMLCILLILGRYFARHKGTYFTHKAGDADAADADATAIINAEQGNNSSEKK 420
DB 379 GVAVVVVVFAMLCILLILGRYFARHKGTYFTHKAGDADAADADATAIINAEQGNNSSEKK 438
QY 421 EYF 423
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Db 439 EYF 441
RESULT 10
ABO07196
ID ABO07196 standard; protein; 442 AA.
XX AC ABO07196;
XX DT 13-AUG-2003 (first entry)
XX DE Human p53 modifying protein, SEQ ID 156.
XX KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
XX KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
XX KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
XX KW apoptotic disorder; cell proliferation disorder.
XX OS Homo sapiens.
XX PN W0200299122-A1.
XX PD 12-DEC-2002.
XX PF 03-JUN-2002; 2002WO-US017382.
XX PR 05-JUN-2001; 2001US-0296076P.
XX PR 10-OCT-2001; 2001US-0328605P.
XX PR 15-FEB-2002; 2002US-0357253P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX WPI; 2003-156859/15.
XX DR N-PSDB; ACD13371.
XX PT Identifying modulators of the p53 pathway for use in treating apoptotic
PT or cell proliferation disorders, comprises screening for agents that
PT modulate activity of a human ortholog of genes that modify the p53
PT pathway in Drosophila.
XX Example 2; Page 469-470; 678pp; English.
XX The invention relates to identifying (M1) a candidate p53 pathway
XX modulating agent, by contacting an assay system comprising a purified HM
XX polypeptide (human orthologue of genes that modify the p53 pathway in
XX Drosophila) or nucleic acid with a test agent under conditions, where but
XX for the presence of the test agent, the system provides a reference
XX activity, and detecting a test agent-biased activity of the assay system.
XX Also included are modulating (M2) a p53 pathway of a cell (comprising
XX contacting a cell defective in p53 function with a candidate modulator
XX that specifically binds to a HM polypeptide comprising an HM amino acid
XX sequence, where p53 function is restored), modulating (M3) a p53 pathway
XX in a mammalian cell (comprising contacting the cell with an agent that
XX specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
XX a disease in a patient (comprising: (a) obtaining a biological sample
XX from the patient; (b) contacting the sample with a probe for HM
XX expression; (c) comparing the results with a control; and (d) determining
XX whether the comparison indicates a likelihood disease). (M1) is useful
XX for identifying modulators of the p53 pathway. A probe for HM expression
XX is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
XX in a patient, where the cancer has greater than 25 % expression level.
XX Modulators identified by (M1) are useful in a variety of diagnostic and
XX therapeutic applications, where disease or disorder prognosis is related
XX to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
XX proliferation disorders (e.g. cancer). Another two new methods (M2 and
XX M3) are useful for modulating the p53 pathway of a cell, thus restoring
XX the p53 function of the cell, so that the cell undergoes normal
XX proliferation or progression through the cell cycle. (M2) and (M3) are
XX also useful for treating defects in the p53 pathway such as angiogenic,
XX apoptotic or cell proliferation disorders. The present sequence
```

139 TVLVPPRLMIDIQKTAVEGEIEVNTCTAMASKPATIRFKGNTLKGSEVEEWSDM 198
181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
241 EGDAPFELTCEAIGKPGQPMVMTWVRVDDDEMPQHAVLSGNPLFNNLKTNDGTYRCEASNI 300
259 EGDALFELTCEAIGKPGQPMVMTWVRVDDDEMPQHAVLSGNPLFNNLKTNDGTYRCEASNI 318
301 VGKASDVMYLVYDPTTIPPTTT 360
319 VGKASDVMYLVYDPTTIPPTTT 378
361 GVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
379 GVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 438
421 EYF 423
439 EYF 441

RESULT 8
ADE54238
ID ADE54238 standard; protein; 442 AA.
XX AC ADE54238;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein NP_055148, SEQ ID NO 41.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WC2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GHEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; NP_055148.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

Query Match 98.7%; Score 2169; DB 7; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.1e-149;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGRLRLRLLLLSAALIPITGDGQNLFTKDVTVIEGEVATISQVNVKSDSDSVIQLLN 60
Db 19 AAPPGRLRLRLLLLSAALIPITGDGQNLFTKDVTVIEGEVATISQVNVKSDSDSVIQLLN 78
QY 61 PNRQTYFRDPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
Db 79 PNRQTYFRDPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 138
QY 121 TVLVPPRLMIDIQKTAVEGEIEVNTCTAMASKPATIRFKGNTLKGSEVEEWSDM 180
Db 139 TVLVPPRLMIDIQKTAVEGEIEVNTCTAMASKPATIRFKGNTLKGSEVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKPGQPMVMTWVRVDDDEMPQHAVLSGNPLFNNLKTNDGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKPGQPMVMTWVRVDDDEMPQHAVLSGNPLFNNLKTNDGTYRCEASNI 318
QY 301 VGKASDVMYLVYDPTTIPPTTT 360
Db 319 VGKASDVMYLVYDPTTIPPTTT 378
QY 361 GVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 420
Db 379 GVVAVVVFAMLCILILGRYFARHKGTYFTHEAKGADDAADATAIINAEQQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 9
ADE86685
ID ADE86685 standard; protein; 442 AA.
XX AC ADE86685;
XX DT 29-JAN-2004 (first entry)
XX DE Novel human secreted protein #11 associated protein #1.
XX KW human; secreted protein; cancer; liver disorder; hepatitis;
XX KW neural disorder; Alzheimer's disease.
XX OS Homo sapiens.
XX PN US2003129685-A1.

Db 439 EYF 441

RESULT 5
AAE19887
ID AAE19887 standard; protein; 442 AA.
XX
AC AAE19887;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
XX
KW Human; hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
KW liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200214557-A1.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025690.
XX
PR 15-AUG-2000; 2000US-0225264P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Reeves RH, Yoshinori M;
XX
DR WPI; 2002-241913/29.
XX
XX
XX Detecting cell proliferative disorder associated with tumor suppressor
XX lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell
XX of subject with reagent detecting TSLC1 and detecting modification in
XX TSLC1 level.
XX
XX Disclosure; Page 49-50; 59pp; English.
XX
XX The invention relates to a method for detecting cell proliferative
XX disorder associated with tumour suppressor lung cancer 1 (TSLC1) in a
XX subject. The method comprising contacting a cell component of a
XX proliferating cell with a reagent that detects level of the cell
XX component in the proliferating cell and determining modification in the
XX level of the cell component in proliferating cell as compared with a
XX healthy cell, where modification indicates disorder associated with a
XX TSLC1. The method is useful for detecting a cell proliferative disorder
XX (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor
XX lung cancer 1 (TSLC1) in a subject. The invention is useful in gene
XX therapy and for treating a cell proliferative disorder such as lung
XX cancer (human non-small cell lung cancer), liver cancer (hepatocellular
XX carcinoma) or pancreatic cancer associated with modification of TSLC1
XX production, where a reagent which modulates (preferably, increases) TSLC1
XX level in the cells, is employed. The present sequence is human TSLC1
XX
XX Sequence 442 AA;
XX
Query Match 98.7%; Score 2169; DB 5; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.1e-149;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
1 AAPPGLRLRLLLLSAALIFTGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
19 AAPPGLRLRLLLLSAALIFTGQGNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
XX
61 PNRQIYFRDFRPLKDSRFLNFSSELKVLSTNVISDEGRYFCQLYTDPPQESYITI 120
79 PNRQIYFRDFRPLKDSRFLNFSSELKVLSTNVISDEGRYFCQLYTDPPQESYITI 138
XX
121 TVLVPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWPKGNKELKGKSEVEWSDM 180
139 TVLVPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWPKGNKELKGKSEVEWSDM 198
XX

191 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTCNLOTORYLEVQYKPOVHIQMTYPLQGLTR 240
199 YTVTSQMLKVKHEDDGVPIVCQVEHPAVTCNLOTORYLEVQYKPOVHIQMTYPLQGLTR 258
241 EGDALFELTCEAIGKPPQPMVTWVRVDDDEMPHVLSPNLFNNLTKDNTCTYCEASNI 300
259 EGDALFELTCEAIGKPPQPMVTWVRVDDDEMPHVLSPNLFNNLTKDNTCTYCEASNI 318
301 VGKASDYMLYVDDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
319 VGKASDYMLYVDDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
361 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAGGGQNNSEKK 420
379 GVAVVVFAMLCILLIILGRYFARHKGTYFTHKAGDADAADATAIINAGGGQNNSEKK 438
421 EYF 423
439 EYF 441

RESULT 6
ABP62825
ID ABP62825 standard; protein; 442 AA.
XX
AC ABP62825;
XX
DT 14-OCT-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 262.
XX
XX
XX Human; vulnary; dermatological; neuroprotective; nootropic; cancer;
XX antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
XX antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
XX burn; central nervous system disorder; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; immune disorder;
XX autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
XX Homo sapiens.
XX
XX WO200218424-A2.
XX
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US027093.
XX
XX 01-SEP-2000; 2000US-00654935.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
XX WPI; 2002-583321/62.
XX
XX N-PSDB; ABQ93304.
XX
XX New polynucleotide and polypeptides, useful for treatment and diagnosis
XX of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
XX sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
XX sclerosis, diabetes and allergies.
XX
XX Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising one of
XX 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
XX administering to a mammalian subject a composition comprising the protein
XX (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
XX (I), (II) and (III) are useful for diagnostic evaluation of disorders.
XX (I) is useful for gene therapy of diseases and (II) can be used for
XX therapeutic treatment. Diseases that may be treated include wound healing
XX and tissue repair, burns, central nervous system disorders (e.g.
XX Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral

QY 61 PNRTIYFRDFRPLKDSRFQQLNFSSELKSVLTVNSISDEGRYFCQLYTDPPOESYTTI 120
Db 79 PNRTIYFRDFRPLKDSRFQQLNFSSELKSVLTVNSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRLMIDIQDVAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPPRLMIDIQDVAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVLEQYKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVLEQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGNFLFINNLTNDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGNFLFINNLTNDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVWFAMLCIIILGRYFARHKGTYFTHAEKAGDADAADTAIINAEQGQNNSEKK 420
Db 379 GVAVVWFAMLCIIILGRYFARHKGTYFTHAEKAGDADAADTAIINAEQGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 4
AAY45092
ID AAY45092 standard; protein; 442 AA.
AC AAY45092;
DT 31-MAY-2000 (first entry)
XX Human lymphoid derived dendritic cell adhesion molecule.
XX Lymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
KW B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
KW biological activity; quality control reagent; treatment; inflammation;
KW immune system disorder; autoimmune; viral infection; infectious disease;
KW organ transplant rejection; bone marrow; modulator; immune response.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..374
FT /label= Extracellular_domain
FT Peptide 1..38
FT /label= Leader_peptide
FT Protein 39..442
FT /label= Mature_human_LDCAM_polypeptide
FT Modified-site 67..69
FT /note= "N-Glycosylation site"
FT Modified-site 101..103
FT /note= "N-Glycosylation site"
FT Modified-site 113..115
FT /note= "N-Glycosylation site"
FT Modified-site 165..167
FT /note= "N-Glycosylation site"
FT Modified-site 304..306
FT /note= "N-Glycosylation site"
FT Modified-site 308..310
FT /note= "N-Glycosylation site"
FT Domain 375..395
FT /label= Transmembrane_domain
FT Domain 396..442
FT /label= Cytoplasmic_domain
PN WO200008158-A2.

XX 17-FEB-2000.
PD
XX
PF 05-AUG-1999; 99WO-US017905.
XX
PR 07-AUG-1998; 98US-0095672P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC;
XX WPI; 2000-205712/18.
DR N-PSDB; AAZ50882.
DR
XX Novel molecules designated LDCAM are capable of altering or modulating T
PT cell function.
XX
PS Claim 7; Page 42-43; 44pp; English.
XX
CC The present amino acid sequence is the human lymphoid derived dendritic
CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
CC region of B7-L1. Human LDCAM is expressed in breast, retina, foetal
CC liver, spleen and heart, lung, muscle, placenta, thyroid and lung
CC carcinoma. LDCAM polypeptides interacts with T cell surface molecules to
CC alter signalling and inhibits T cell proliferation, bind to themselves
CC and B7-L1, an LDCAM binding protein and increases natural killer (NK)
CC cell populations. It may be used to measure the biological activity and
CC as quality control reagents of LDCAM binding proteins. LDCAM may be used
CC for treating disorders associated with malfunctioning of immune system,
CC inflammation, autoimmune disorders, viral infected cells, infectious
CC diseases and for killing tumour cells. They are also useful for
CC prevention or reducing the effect of organ and bone marrow transplant
CC rejection and for modulating T cell immune responses. LDCAM polypeptides
CC may also be used as carriers for delivering agents attached to T cells or
CC cells bearing B7L-1
XX
SQ Sequence 442 AA;
Query Match 98.7%; Score 2169; DB 3; Length 442;
Best Local Similarity 98.8%; Pred. No. 2.1e-149;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLLLLSAALIPITGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
Db 19 AAPPGLRLRLLLLSAALIPITGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
QY 61 PNRTIYFRDFRPLKDSRFQQLNFSSELKSVLTVNSISDEGRYFCQLYTDPPOESYTTI 120
Db 79 PNRTIYFRDFRPLKDSRFQQLNFSSELKSVLTVNSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRLMIDIQDVAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPPRLMIDIQDVAVEGEIEVNCCTAMASKPATTIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVLEQYKPOVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTVLEQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGNFLFINNLTNDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKPPQPMVTVWRVDDMPQHAVLSGNFLFINNLTNDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVWFAMLCIIILGRYFARHKGTYFTHAEKAGDADAADTAIINAEQGQNNSEKK 420
Db 379 GVAVVWFAMLCIIILGRYFARHKGTYFTHAEKAGDADAADTAIINAEQGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

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Qy 121 TVLPPRLMIDIQKTAVEGEEIEVNTAKSPATTIRWFKGNKELKGKSEVEEWSDM 180
Db 139 TVLPPRLMIDIQKTAVEGEEIEVNTAKSPATTIRWFKGNKELKGKSEVEEWSDM 198
Qy 181 YTVTSQMLKVKHEDDGVFVICOVEHPAVTGNLQRYLEVQYKPOVHIQNTYPLQGLTR 240
Db 199 YTVTSQMLKVKHEDDGVFVICOVEHPAVTGNLQRYLEVQYKPOVHIQNTYPLQGLTR 258
Qy 241 EGDAPFELTCEAIGKPOPMVWTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKPOPMVWTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
Qy 301 VGKAHSDVMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKAHSDVMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
Qy 361 GVAVVVFVFMILCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEQGQNNSEKK 420
Db 379 GVAVVVFVFMILCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEQGQNNSEKK 438
Qy 421 EYF 423
Db 439 EYF 441

RESULT 3
AAY94341
ID AAY94341 standard; protein; 442 AA.
XX AC AAY94341;
XX DT 22-AUG-2000 (first entry)
XX DE Human cell surface receptor protein #8.
XX KW Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
KW Alzheimer's diseases; multiple sclerosis; epilepsy.
XX OS Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX Peptide 1..44
XX Protein 45..442
XX Region 53
XX Domain 57..126
XX Region /label= Immunoglobulin_domain
XX Region /note= "potential glycosylation site"
XX Region 101
XX Region /note= "potential glycosylation site"
XX Region 103
XX Region /note= "potential glycosylation site"
XX Region 113
XX Region /note= "potential glycosylation site"
XX Region 115
XX Region /note= "potential glycosylation site"
XX Region 155
XX Region /note= "potential glycosylation site"
XX Domain 159..222
XX Region /label= Immunoglobulin_domain
XX Region 165
XX Region /note= "potential glycosylation site"
XX Region 176
XX Region /note= "potential glycosylation site"
XX Region 190
XX Region /note= "potential glycosylation site"
XX Region 233

```

```

FT Region /note= "potential phosphorylation site"
FT 241
FT Domain /note= "potential phosphorylation site"
FT 260..315
FT Region /label= Immunoglobulin_domain
FT 304
FT Region /note= "potential glycosylation site"
FT 308
FT Region /note= "potential glycosylation site"
FT 310
FT Region /note= "potential phosphorylation site"
FT 329
FT Region /note= "potential phosphorylation site"
FT 368
FT Domain /note= "potential phosphorylation site"
FT 375..394
FT Region /label= Transmembrane_domain
FT 432
FT /note= "potential glycosylation site"

```

WO200028032-A2.

18-MAY-2000.

12-NOV-1999; 99WO-US026742.

12-NOV-1998; 98US-00191280.

07-DEC-1998; 98US-00206647.

08-MAR-1999; 99US-0123404P.

(INCY-) INCYTE PHARM INC.

Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;

Hillman JL, Bandman O, Azimzai Y, Au-Young J;

MPI; 2000-376546/32.

N-PSDB; AAA27051.

New human cell surface receptor protein and polynucleotide useful for

diagnosis, prevention and treatment of cancer, immune disorders,

infection and neuronal disorders.

Claim 1; Page 81-82; 97pp; English.

The present sequence is a novel human cell surface receptor protein (HCSR) designated HCSR-8. The nucleotide sequence was identified in Incyte Clone 312256 from the cDNA library LUNGNOT02, which was made from RNA isolated from lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 93779242. HCSR and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSR. Such disorders include cancers such as leukaemia and melanoma, immune bacterial and parasitic infections and neuronal disorders such as akathesia, Alzheimer's disease, multiple sclerosis and epilepsy. CC Polynucleotides encoding HCRPs may be used as hybridisation probes to diagnose these conditions. Anti-HCSR antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSR and for diagnosis of HCSR-related disorders. HCSR and its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds

Sequence 442 AA;

Query Match 98.7%; Score 2169; DB 3; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAPPGLRLRLLLLSAAALIPFGDGNLFTKDVIEGEVATISCVNKSDDSVIQLN 60
 Db 15 AAPPGLRLRLLLLSAAALIPFGDGNLFTKDVIEGEVATISCVNKSDDSVIQLN 78

PI Baum PR, Fanslow WC;
 XX WPI: 2000-205712/18.
 DR N-PSDB; AAZ50883.
 XX Novel molecules designated LDCAM are capable of altering or modulating T
 PT cell function.
 XX
 PS Claim 7; Page 46-47; 44pp; English.
 XX
 CC The present amino acid sequence is the mouse lymphoid derived dendritic
 CC cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic
 CC cells and displays homology to adhesion molecules, B7-1 and cytoplasmic
 CC region of B7-L1. Mouse LDCAM is found on whole embryo, testes, triple
 CC negative cells murine splenic and lymph node CD8+, S49.1 and dendritic
 CC cells. LDCAM polypeptides interact with T cell surface molecules to
 CC alter signalling and inhibits T cell proliferation, bind to themselves
 CC and B7L-1, an LDCAM binding protein and increases natural killer (NK)
 CC cell populations. It may be used to measure the biological activity and
 CC as quality control reagents of LDCAM binding proteins. LDCAM may be used
 CC for treating disorders associated with malfunctioning of immune system,
 CC inflammation, autoimmune disorders, viral infected cells, infectious
 CC diseases and for killing tumour cells. They are also useful for
 CC prevention or reducing the effect of organ and bone marrow transplant
 CC rejection and for modulating T cell immune responses. LDCAM polypeptides
 CC may also be used as carriers for delivering agents attached to T cells or
 CC cells bearing B7L-1
 XX
 SQ Sequence 423 AA;

Query Match 100.0%; Score 2197; DB 3; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.8e-151;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 DB 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 QY 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYDPPQESYTTI 120
 DB 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYDPPQESYTTI 120
 QY 121 TVLVPPRNLMIDIQKTAVEGEIEVNCATAMASKPATTIRFWFGNKELKKGSEVEWSDM 180
 DB 121 TVLVPPRNLMIDIQKTAVEGEIEVNCATAMASKPATTIRFWFGNKELKKGSEVEWSDM 180
 QY 181 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQOTRYLEVOYKPVQHIQMTYFLOGLTR 240
 DB 181 YTVTSQMLKVKHEDDGPVICOVEHPAVTGNLQOTRYLEVOYKPVQHIQMTYFLOGLTR 240
 QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSPGNLFINLNKTDNGTYRCEASNI 300
 DB 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSPGNLFINLNKTDNGTYRCEASNI 300
 QY 301 VGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
 DB 301 VGKAHSDYMLVYDPPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
 QY 361 GVAVVVVFMCLLLIILGRYFARHKGTYFTHEAKGADDAADADATATINAEQGNNEEKK 420
 DB 361 GVAVVVVFMCLLLIILGRYFARHKGTYFTHEAKGADDAADADATATINAEQGNNEEKK 420
 QY 421 EYF 423
 DB 421 EYF 423

RESULT 2
 AAB25619
 ID AAB25619 standard; protein; 442 AA.
 XX
 AC AAB25619;
 XX

DT 21-NOV-2000 (first entry)
 XX Protein encoded by human secreted protein gene #11.
 DE
 XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
 KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
 KW anticancer; vulnary; antiviral; antibacterial; antifungal;
 KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
 KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
 KW Crohn's disease; nephritis; hyperproliferative disorder;
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
 KW melanoma; lymphoma; wound healing; human.
 XX
 OS Homo sapiens.
 XX WO200029435-A1.
 XX 25-MAY-2000.
 XX 27-OCT-1999; 99WO-US025031.
 XX 28-OCT-1998; 98US-0105971P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
 PI Greene JM;
 PI WPI: 2000-387742/33.
 DR
 XX Isolated nucleic acid molecules encoding human secreted proteins are used
 XX for the prevention, amelioration and treatment of autoimmune,
 XX inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 XX wounds, and infectious diseases.
 XX Disclosure; Page 182-183; 803pp; English.
 XX The present invention relates to 12 secreted human proteins and the
 XX nucleotide sequences encoding them. The polynucleotide sequences given in
 XX AAA80606-A80623 encode the 12 secreted protein sequences given in
 XX AAB25576-B25593. The human secreted proteins have various activities
 XX dependent on the tissues in which they are expressed. Examples of the
 XX activities of the proteins include: immunosuppressant; anti-inflammatory;
 XX antirheumatic; antirheumatic; dermatological; antiproliferative;
 XX antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
 XX and antifungal activity. The proteins, polypeptides, agonists and
 XX antagonists may be used to treat prevent and/or diagnose various disease,
 XX disorders and conditions examples of which include: immune disorders e.g.
 XX Addison's disease, rheumatoid arthritis, dermatitis, and multiple
 XX sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
 XX Crohn's disease and nephritis; hyperproliferative disorders such as
 XX paraproteinemia and purpura; cardiovascular disorders e.g. coronary
 XX arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
 XX proteins and polynucleotide sequences may also be used in wound healing
 XX and the treatment of infectious diseases. The human secreted protein gene
 XX #11 and protein sequences are represented in sequences AAA80616 and
 XX AAB25586. Sequences AAA80677-A80682 represent genes related to the
 XX secreted protein gene#11
 XX Sequence 442 AA;

Query Match 98.7%; Score 2169; DB 3; Length 442;
 Best Local Similarity 98.8%; Pred. No. 2.1e-149;
 Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 60
 DB 19 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLLN 78
 QY 61 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYDPPQESYTTI 120
 DB 79 PNRQTIYFRDFRLKDSRFQLLNFSSSELKSVLTNVSISDEGRYFCQLYDPPQESYTTI 138

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 48.4142 Seconds
(without alignments)
2468.650 Million cell updates/sec

Title: US-09-778-187b-4

Perfect score: 2197

Sequence: 1 APPGLRLRLLLLLLAAAL.....TAINAEGQNNSEKKEYF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Lasting first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	423	3 AAY45093	Aay45093 Mouse Lym
2	2169	98.7	442	3 AAB25619	Aab25619 Protein e
3	2169	98.7	442	3 AAY94341	Aay94341 Human cel
4	2169	98.7	442	3 AAY45092	Aay45092 Human lym
5	2169	98.7	442	5 AAB19887	Aab19887 Human tum
6	2169	98.7	442	5 ABP62825	Abp62825 Human pol
7	2169	98.7	442	6 ADA27144	Ada27144 Human nov
8	2169	98.7	442	7 ADE54238	Ade54238 Human pro
9	2169	98.7	442	8 ABE86685	Abe86685 Novel hum
10	2166	98.6	442	6 ABO07196	Ab007196 Human p53
11	2166	98.6	442	6 ABO07231	Ab007231 Human p53
12	2166	98.6	442	7 ADE61605	Ade61605 Human pro
13	2166	98.6	442	7 ADE61608	Ade61608 Human pro
14	2149	97.8	440	2 AAY17830	Aay17830 Human pro
15	2149	97.8	440	3 AAB01321	Aab01321 Human pro
16	2149	97.8	440	4 AAU29040	Aau29040 Human pro
17	2149	97.8	440	6 ABU58416	Abu58416 Human pro
18	2149	97.8	440	6 ABU87964	Abu87964 Novel hum
19	2149	97.8	440	6 ABU84279	Abu84279 Human sec
20	2149	97.8	440	6 ABR66153	Abr66153 Human sec
21	2149	97.8	440	6 ABR65543	Abr65543 Human sec
22	2149	97.8	440	6 ABU99483	Abu99483 Human sec
23	2149	97.8	440	6 ABU55930	Abu55930 Human sec
24	2149	97.8	440	6 ABU82722	Abu82722 Human pro
25	2149	97.8	440	6 ABU89843	Abu89843 Novel hum

ALIGNMENTS

RESULT 1

AAAY45093

ID AAY45093 standard; protein; 423 AA.

AC AAY45093;

XX

DT 31-MAY-2000 (first entry)

XX

DE Mouse lymphoid derived dendritic cell adhesion molecule.

XX

KW Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1;
B7-1; T cell proliferation; natural killer cell; NK; tumour cell;
biological activity; quality control reagent; treatment; inflammation;
immune system disorder; autoimmune; viral infection; infectious disease;
organ transplant rejection; bone marrow; modulator; immune response.

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Domain 1..356

FT Modified-site /label= Extracellular_domain

FT Modified-site /note= "N-Glycosylation site"

FT Modified-site /note= "N-Glycosylation site"

FT Modified-site /note= "N-Glycosylation site"

FT Modified-site /note= "N-Glycosylation site"

FT Modified-site /note= "N-Glycosylation site"

FT Modified-site /note= "N-Glycosylation site"

FT Modified-site /note= "N-Glycosylation site"

FT Domain /label= Transmembrane_domain

FT Domain /label= Cytoplasmic_domain

XX WO200006158-A2.

XX 17-FEB-2000.

XX 05-AUG-1999; 99WO-US017905.

XX 07-AUG-1998; 98US-0095672P.

XX (IMMV) IMMUNEX CORP.

Abr68092 Human sec
Abu96145 Novel hum
Abu92576 Human sec
Abo08653 Human sec
Abo02705 Human sec
Abr74859 Human sec
Abr94621 Human sec
Abu60240 Human pro
Abu85594 Human pro
Abu98754 Novel hum
Abu91675 Novel hum
Abu89368 Human pro
Abu86209 Human sec
Abu67422 Human sec
Abu80450 Human pro
Abr99368 Human sec
Abr98758 Human sec
Abo16281 Human sec
Abr92181 Human sec

26 2149 97.8 440 6 ABR68092
27 2149 97.8 440 6 ABU96145
28 2149 97.8 440 6 ABU92576
29 2149 97.8 440 6 ABO08653
30 2149 97.8 440 6 ABO02705
31 2149 97.8 440 6 ABR74859
32 2149 97.8 440 6 ABR94621
33 2149 97.8 440 6 ABU60240
34 2149 97.8 440 6 ABU85594
35 2149 97.8 440 6 ABU98754
36 2149 97.8 440 6 ABU91675
37 2149 97.8 440 6 ABU89368
38 2149 97.8 440 6 ABU86209
39 2149 97.8 440 6 ABU67422
40 2149 97.8 440 6 ABU80450
41 2149 97.8 440 6 ABR99368
42 2149 97.8 440 6 ABR98758
43 2149 97.8 440 6 ABO16281
44 2149 97.8 440 6 ABR92181
45 2149 97.8 440 6 ABR92181

Db 199 YTVTSQMLKVKHEDDGVFVVCQVEHPAVTGNLQORYLEVQYKQPQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIGKQPQPMVTVVRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 259 EGDALFELTCEAIGKQPQPMVTVVRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 318
QY 301 VGKASDYMLYVYDPPPTTTPPTTT 360
Db 319 VGKASDYMLYVYDPPPTTTPPTTT 378
QY 361 GVAVVVFAMLCILIIILGRYFARHKGYFTHEAKGADDAADADATAIINAEGGQNNSEKK 420
Db 379 GVAVVVFAMLCILIIILGRYFARHKGYFTHEAKGADDAADADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 15

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 97.8%; Score 2149; DB 9; Length 440;
Best Local Similarity 98.3%; Pred. No. 8.3e-167;
Matches 416; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
QY 1 AAPGRLRLRLLLLSAAALPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
Db 19 AAPPG--LRLLLLFSAALPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 76
QY 61 PNRQTIYFRDPRFKDSRFOLLNPFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
Db 77 PNRQTIYFRDPRFKDSRFOLLNPFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 136
QY 121 TVLVPPRLNLMIDIQKDTAVEGEIEVNCNTAKSPATTIRWFKNKELKGSVEEWSDM 180
Db 137 TVLVPPRLNLMIDIQKDTAVEGEIEVNCNTAKSPATTIRWFKNKELKGSVEEWSDM 196
QY 181 YTVTSQMLKVKHEDDGVFVVCQVEHPAVTGNLQORYLEVQYKQPQVHIQMTYPLQGLTR 240
Db 197 YTVTSQMLKVKHEDDGVFVVCQVEHPAVTGNLQORYLEVQYKQPQVHIQMTYPLQGLTR 256

QY 241 EGDAPFELTCEAIGKQPQPMVTVVRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 257 EGDALFELTCEAIGKQPQPMVTVVRVDDDEMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 316
QY 301 VGKASDYMLYVYDPPPTTTPPTTT 360
Db 317 VGKASDYMLYVYDPPPTTTPPTTT 376
QY 361 GVAVVVFAMLCILIIILGRYFARHKGYFTHEAKGADDAADADATAIINAEGGQNNSEKK 420
Db 377 GVAVVVFAMLCILIIILGRYFARHKGYFTHEAKGADDAADADATAIINAEGGQNNSEKK 436
QY 421 EYF 423
Db 437 EYF 439

Search completed: May 27, 2004, 09:52:21
Job time : 36.9363 secs

US-10-015-115-111
; Sequence 111, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Baha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-111

Query Match 98.7%; Score 2169; DB 15; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLLLLLLSAALIPFGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
DB 19 AAPPGLRLRLLLLLLSAALIPFGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRFKDSRFQNLFFSSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNRQTIYFRDPRFKDSRFQNLFFSSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRLNLMIDIQDRTAVEGEIEVNCMTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 139 TVLVPPRLNLMIDIQDRTAVEGEIEVNCMTAMASKPATIRWFKGNKELKGKSEVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQTVLEVQYKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQTVLEVQYKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEAIKGPQVMTWVRVDDMPQHAVLSGNLFINNKNTDNGTYRCEASNI 300
DB 259 EGDALCELCEAIKGPQVMTWVRVDDMPQHAVLSGNLFINNKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDPTTIPPTTT 360
DB 319 VGKAHSDYMLVYDPTTIPPTTT 378

QY 361 GVVAVVVFAMLCCLLIILGRYFARHKGTFTHEAKGADDAADATATINAEQQNNSEKK 420
DB 379 GVVAVVVFAMLCCLLIILGRYFARHKGTFTHEAKGADDAADATATINAEQQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441
RESULT 14
US-10-015-115-110
; Sequence 110, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Baha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-110
Query Match 98.6%; Score 2166; DB 15; Length 442;
Best Local Similarity 98.6%; Pred. No. 3.4e-168;
Matches 47; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLLLLLLSAALIPFGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
DB 19 AAPPGLRLRLLLLLLSAALIPFGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRFKDSRFQNLFFSSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNRQTIYFRDPRFKDSRFQNLFFSSSELKVSILNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPRLNLMIDIQDRTAVEGEIEVNCMTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 139 TVLVPPRLNLMIDIQDRTAVEGEIEVNCMTAMASKPATIRWFKGNKELKGKSEVEEWSDM 198
QY 181 YTVTSQMLKVKHEDDGPVVICQVEHPAVTGNLQTVLEVQYKQVHIQMTYPLQGLTR 240

QY 121 TVLVPPRNLMDIQDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSM 180
DB 139 TVLVPPRNLMDIQDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVKHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKQPQPMVMTWVRVDDMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKQPQPMVMTWVRVDDMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHAVID 360
DB 319 VGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHAVID 378
QY 361 GVAVVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADATTAIINAEAGGQNNSEKK 420
DB 379 GVAVVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADATTAIINAEAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 11

US-10-302-041-20
; Sequence 20, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLSAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
DB 19 AAPGLRLRLLLLSAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPPRNLMDIQDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSM 180
DB 139 TVLVPPRNLMDIQDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVKHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKQPQPMVMTWVRVDDMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKQPQPMVMTWVRVDDMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 318

QY 301 VGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHAVID 360
DB 319 VGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHAVID 378
QY 361 GVAVVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADATTAIINAEAGGQNNSEKK 420
DB 379 GVAVVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADATTAIINAEAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 12

US-10-403-107-1
; Sequence 1, Application US/10403107
; Publication No. US20030165974A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINO, Mutsaers
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHUI770-1
; CURRENT APPLICATION NUMBER: US/10/403,107
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US/09/930,803
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-107-1

Query Match 98.7%; Score 2169; DB 14; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPGLRLRLLLLSAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
DB 19 AAPGLRLRLLLLSAALIPDQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
DB 79 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 138
QY 121 TVLVPPRNLMDIQDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSM 180
DB 139 TVLVPPRNLMDIQDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVKHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGVFVICQVEHPAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258
QY 241 EGDALFELTCEAIGKQPQPMVMTWVRVDDMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 300
DB 259 EGDALFELTCEAIGKQPQPMVMTWVRVDDMPQHAVLSGNLFINNLKNTDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHAVID 360
DB 319 VGKAHSDYMLVYVDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTITDTSRAGEEGTIGAVDHAVID 378
QY 361 GVAVVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADATTAIINAEAGGQNNSEKK 420
DB 379 GVAVVVVFAMCLLLIILGRYFARHKGTYFTHEAKGADDAADATTAIINAEAGGQNNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 13

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; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patent In Ver. 2.0
; LENGTH: 442
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-984-130-136

Query Match
Best Local Similarity 98.7%; Score 2169; DB 10; Length 442;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLLLSAAALPTGQGNLFKDVTVIEGEVATISCVNKSDDSVIQLLN 60
DB 19 AAPPLRLRLLLLLLSAAALPTGQGNLFKDVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRTIYFRDFRPLKDSRFQLLNFSSSELKVSNTNSISDEGRYFCOLYTDPQESYTTI 120
DB 79 PNRTIYFRDFRPLKDSRFQLLNFSSSELKVSNTNSISDEGRYFCOLYTDPQESYTTI 138
QY 121 TVLVPPRNLMIDIOKD TAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEEWSM 180
DB 139 TVLVPPRNLMIDIOKD TAVEGEEIEVNCTAMASKPATIRFWKGNKELKGKSEVEEWSM 198
QY 181 YTVTSQMLKVHKEDDGPVICQVEHPAVTGNLTQRYLEVQYKPQHIOMTYPLOGLTR 240
DB 199 YTVTSQMLKVHKEDDGPVICQVEHPAVTGNLTQRYLEVQYKPQHIOMTYPLOGLTR 258
QY 241 EGDAPFLTCEAIGKQPVMVTWVRVDDMPQHAVLSPNFLFINNLKTDNGTYRCASNI 300
DB 259 EGDALELTCEAIGKQPVMVTWVRVDDMPQHAVLSPNFLFINNLKTDNGTYRCASNI 318
QY 301 VGKAHSDYMLXYVDPPPTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 319 VGKAHSDYMLXYVDPPPTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVVVFAMLCLLIIILGRYFARHGKYTFHEAKGADDAADADATAIINAEGGONNSEKK 420
DB 379 GVAVVVVFAMLCLLIIILGRYFARHGKYTFHEAKGADDAADADATAIINAEGGONNSEKK 438
QY 421 EYF 423
DB 439 EYF 441

RESULT 9
US-09-836-353A-136
; Sequence 136, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P1
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 136

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Db 300 EGDFAELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 359
QY 301 VGKAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
Db 360 VGKAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 419
QY 350 TIGAVDHAVIGGVAVVVFVAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINA 409
Db 420 TIGAVDHAVIGGVAVVVFVAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINA 479
QY 410 EGGQNNSEKKEYF 423
Db 480 EGGQNNSEKKEYF 493

RESULT 6

US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-778-510-20

Query Match 98.7%; Score 2169; DB 9; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLLLLLSAAALIPGTGQNLFTKQVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPPGLRLRLLLLLSAAALIPGTGQNLFTKQVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 120
Db 79 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPNLMIDIQKTAVGEIEVNCCTAMASKPATTTIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPPNLMIDIQKTAVGEIEVNCCTAMASKPATTTIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLVKHKKEDDGPVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLVKHKKEDDGPVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 258
QY 241 EGDFAELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
Db 259 EGDFAELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVVFVAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEKK 420
Db 379 GVAVVVFVAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

RESULT 8

US-09-984-130-136
; Sequence 136, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PP489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792

RESULT 7
US-09-778-187B-2
; Sequence 2, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 442
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2

Query Match 98.7%; Score 2169; DB 9; Length 442;
Best Local Similarity 98.8%; Pred. No. 2e-168;
Matches 418; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLLLLLSAAALIPGTGQNLFTKQVTVIEGEVATISCVNKSDDSVIQLLN 60
Db 19 AAPPGLRLRLLLLLSAAALIPGTGQNLFTKQVTVIEGEVATISCVNKSDDSVIQLLN 78
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 120
Db 79 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSLSLTVNSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPNLMIDIQKTAVGEIEVNCCTAMASKPATTTIRWFKGNKELKGKSEVEWSDM 180
Db 139 TVLVPPNLMIDIQKTAVGEIEVNCCTAMASKPATTTIRWFKGNKELKGKSEVEWSDM 198
QY 181 YTVTSQMLVKHKKEDDGPVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
Db 199 YTVTSQMLVKHKKEDDGPVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 258
QY 241 EGDFAELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 300
Db 259 EGDFAELTCEAIGKQPQVMVTVRVDDEMPQHAVLSGNLFINNLTNDNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
Db 319 VGKAHSDYMLVYDDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 361 GVAVVVFVAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEKK 420
Db 379 GVAVVVFVAMLCCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEKK 438
QY 421 EYF 423
Db 439 EYF 441

GENERAL INFORMATION:

APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesha
APPLICANT: Gangolli, Esha A
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 112
LENGTH: 445
TYPE: PRT
ORGANISM: Mus musculus
US-10-015-115-112

Query Match 100.0%; Score 2197; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1e-170;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
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DB 82 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 141
QY 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 142 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 201
QY 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
DB 202 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEAIGKQPVMVTVRVDDEMPQHAVLSGNPLFINNKNKTNGTYRCEASNI 300
DB 262 EGDAPFELTCEAIGKQPVMVTVRVDDEMPQHAVLSGNPLFINNKNKTNGTYRCEASNI 321
QY 301 VQKASDVMYLVYDPTTTPPTTT 360
DB 322 VQKASDVMYLVYDPTTTPPTTT 381
QY 361 GYVAVVVFAMCLLIILGRYFARHKGTYFTEAKGADDAADATAIINAEQGNNSSEKK 420
DB 382 GYVAVVVFAMCLLIILGRYFARHKGTYFTEAKGADDAADATAIINAEQGNNSSEKK 441

QY 421 EYF 423
DB 442 EYF 444

RESULT 5

US-10-015-115-113
Sequence 113, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesha
APPLICANT: Gangolli, Esha A
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 113
LENGTH: 494
TYPE: PRT
ORGANISM: Mus musculus
US-10-015-115-113

Query Match 99.1%; Score 2176.5; DB 15; Length 494;
Best Local Similarity 97.2%; Pred. No. 5.6e-169;
Matches 422; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

QY 1 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
DB 60 AAPPGLRLRLLLLSAAALPTGQNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 119
QY 61 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 120
DB 120 PNRQTIYFRDPRPLKDSRFQQLNFSSELKVSILTNVSIISDEGRYFCQLYTDPPQESYTTI 179
QY 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
DB 180 TVLVPPRNLMIDIQKDTAVEGEEIEVNCVTAMASKPATIRWFKGNKELKGKSEVEEWSDM 239
QY 181 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 240
DB 240 YTVTSQMLKVKHEDDGVPIQVHEPAVTGNLQRYLEVQYKPVQVHIQMTYPLQGLTR 299
QY 241 EGDAPFELTCEAIGKQPVMVTVRVDDEMPQHAVLSGNPLFINNKNKTNGTYRCEASNI 300

QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
Db 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
QY 301 VGKASHDYMLYVDDPTTTPPTTT 360
Db 301 VGKASHDYMLYVDDPTTTPPTTT 360
QY 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
Db 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423
RESULT 2
US-09-778-187B-4
; Sequence 4, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: US 60/095,672
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: mus musculus
US-09-778-187B-4
Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.6e-171;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLMLLLSAAALIPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
Db 1 AAPPGLRLRLMLLLSAAALIPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
Db 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEBWSM 180
Db 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEBWSM 180
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
Db 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
QY 301 VGKASHDYMLYVDDPTTTPPTTT 360
Db 301 VGKASHDYMLYVDDPTTTPPTTT 360
QY 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
Db 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423

Db 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423
RESULT 3
US-10-302-041-22
; Sequence 22, Application US/10302041
; Publication No. US20030144478A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B71l
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/10/302,041
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-302-041-22
Query Match 100.0%; Score 2197; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.6e-171;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPPGLRLRLMLLLSAAALIPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
Db 1 AAPPGLRLRLMLLLSAAALIPTGQGNLFTKDVTVIEGEVATISQVKNKSDSDSVIQLLN 60
QY 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
Db 61 PNRQTIYFRDPRPLKDSRFQLLNFSSSELKVSILTNVSIISDEGRYFCOLYTDPPQESYTTI 120
QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEBWSM 180
Db 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCNTAMASKPATIRWFKGNKELKGKSEVEBWSM 180
QY 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
Db 181 YTVTSQMLKVKHEDDGVPIQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
QY 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
Db 241 EGDAPFELTCEAIGKQPQVMTWVRVDDMPQHAVLSGPNLFINNKNKTNDNGTYRCEASNI 300
QY 301 VGKASHDYMLYVDDPTTTPPTTT 360
Db 301 VGKASHDYMLYVDDPTTTPPTTT 360
QY 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
Db 361 GVAVVVFAMCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEQGQNNSEKK 420
QY 421 EYF 423
Db 421 EYF 423
RESULT 4
US-10-015-115-112
; Sequence 112, Application US/10015115
; Publication No. US20030207800A1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 35.9363 Seconds
(without alignments)

3286.999 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPPGRLRLLLLLLSAAAL.....TAIINAEGQNNSEKKEYF 423

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2197	100.0	423	9	US-09-778-510-22
2	2197	100.0	423	9	US-09-778-187B-4
3	2197	100.0	423	14	US-10-302-041-22
4	2197	100.0	445	15	US-10-015-115-112
5	2176.5	99.1	494	15	US-10-015-115-113
6	2169	98.7	442	9	US-09-778-510-20
7	2169	98.7	442	9	US-09-778-187B-2
8	2169	98.7	442	10	US-09-984-130-136
9	2169	98.7	442	10	US-09-836-353A-136
10	2169	98.7	442	12	US-10-363-616-262
11	2169	98.7	442	14	US-10-302-041-20
12	2169	98.7	442	14	US-10-403-107-1
13	2169	98.7	442	15	US-10-015-115-111
14	2166	98.6	442	15	US-10-015-115-110
15	2149	97.8	440	9	US-09-866-028-61

16	2149	97.8	440	9	US-09-944-449-61	Sequence 61, Appl
17	2149	97.8	440	9	US-09-944-457-61	Sequence 61, Appl
18	2149	97.8	440	9	US-09-944-862-61	Sequence 61, Appl
19	2149	97.8	440	9	US-09-945-587-61	Sequence 61, Appl
20	2149	97.8	440	9	US-09-945-587-61	Sequence 61, Appl
21	2149	97.8	440	9	US-09-944-396-61	Sequence 61, Appl
22	2149	97.8	440	9	US-09-944-097-61	Sequence 61, Appl
23	2149	97.8	440	9	US-09-944-432-61	Sequence 61, Appl
24	2149	97.8	440	9	US-09-943-762-61	Sequence 61, Appl
25	2149	97.8	440	9	US-09-944-654-61	Sequence 61, Appl
26	2149	97.8	440	9	US-09-943-851A-61	Sequence 61, Appl
27	2149	97.8	440	9	US-09-944-413-61	Sequence 61, Appl
28	2149	97.8	440	9	US-09-944-403-61	Sequence 61, Appl
29	2149	97.8	440	9	US-09-944-896-61	Sequence 61, Appl
30	2149	97.8	440	9	US-09-944-944-61	Sequence 61, Appl
31	2149	97.8	440	9	US-09-944-929-61	Sequence 61, Appl
32	2149	97.8	440	9	US-09-944-907-61	Sequence 61, Appl
33	2149	97.8	440	10	US-09-944-884-61	Sequence 61, Appl
34	2149	97.8	440	10	US-09-944-852-61	Sequence 61, Appl
35	2149	97.8	440	10	US-09-943-780-61	Sequence 61, Appl
36	2149	97.8	440	11	US-09-945-584-61	Sequence 61, Appl
37	2149	97.8	440	12	US-10-208-915-34	Sequence 34, Appl
38	2149	97.8	440	12	US-10-199-670-34	Sequence 34, Appl
39	2149	97.8	440	12	US-10-201-858-34	Sequence 34, Appl
40	2149	97.8	440	12	US-10-205-890-34	Sequence 34, Appl
41	2149	97.8	440	12	US-10-208-024-34	Sequence 34, Appl
42	2149	97.8	440	12	US-10-201-853-34	Sequence 34, Appl
43	2149	97.8	440	12	US-10-677-471-61	Sequence 61, Appl
44	2149	97.8	440	12	US-10-677-669-61	Sequence 61, Appl
45	2149	97.8	440	12	US-10-174-581-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

Query Match 100.0%; Score 2197; DB 9; Length 423;
Best Local Similarity 100.0%; Pred. No. 9.6e-171; Indels 0; Gaps 0;
Matches 423; Conservative 0; Mismatches 0;

QY	1	AAPPGRLRLLLLLLSAAALFTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLIN	60
Db	1	AAPPGRLRLLLLLLSAAALFTGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLIN	60
QY	61	PNRQIYFRDPRPLKDSRFQLINFSSELKVSILTNVSIISDEGRYFCOLYTDPPQSYTTI	120
Db	61	PNRQIYFRDPRPLKDSRFQLINFSSELKVSILTNVSIISDEGRYFCOLYTDPPQSYTTI	120
QY	121	TVLVPRNLIMIDIQKDTAVEGEIEVNCVTAMASKATTIRWFKGNKELKGKSEVEWSDM	180
Db	121	TVLVPRNLIMIDIQKDTAVEGEIEVNCVTAMASKATTIRWFKGNKELKGKSEVEWSDM	180

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Db 61 KVHEDDGPVVCQVHEPAVTGNLTQRYLEVQYKQPQVHIQMTYPLQGLTREGDALELTC 120
QY 250 EAIGKPOQVMVTVWRVDDMEQHAVLSGNPLFINNLANKTNGTYRCEASNIVGKAHSDYM 309
Db 121 EAIGKPOQVMVTVWRVDDMEQHAVLSGNPLFINNLANKTNGTYRCEASNIVGKAHSDYI 180
QY 310 LYVYDPTTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAVIGGVAVVVFA 369
Db 181 LYVYD-----TTATTEPAVHDSRAGEEGTIGAVDHAVIGGVAVVVFA 223
QY 370 MLCILLILGRYFARHKGTYFTHKAGDAADADATAIINAEAGQNNSEKKEYF 423
Db 224 MLCILLILGRYFARHKGTYFTHKAGDAADADATAIINAEAGQNNSEKKEYF 277

RESULT 15
Q8N3J6
ID Q8N3J6 PRELIMINARY; PRT; 435 AA.
AC Q8N3J6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKZP761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgam;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 40.8%; Score 897; DB 4; Length 435;
Best Local Similarity 44.2%; Pred. No. 1.5e-67;
Matches 192; Conservative 75; Mismatches 139; Indels 28; Gaps 7;

QY 11 LLLLLSAAALIPTC-DGQNLFTKDVTVIEGEVATISQVKNKSDSVIQLNPNRQTIYFR 69
Db 8 VLRFSVCGLLSQSQGFPLTQNVTVVEGGTALTCTRDNDNTSLQWSNPAQQTLYFD 67
QY 70 DFRPLKDSRFQLNLFSSSELKVLSTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPNL 129
Db 68 DKXALDRNRIELVRASWHELISVSDVSDDEGQYTCSLFTMPVKTSKAYLTVLGVPEKP 127
QY 130 MIDIQKDTAVEGEEIEVNCAMASKPATTIRWPKGNKELKGKSEVEWS---DMYTVTSQ 186
Db 128 QISGFSSPVNMEGLMQLTCKTSGSKPAADIRWFKNDKEIKDVLYKLEEDANRKTFTVSST 187
QY 187 LMLKVHKDDGVPVICQVEHPATGNLQ-TQRYLEVQYKQPQVHIQMTYPLQGLTRGDFAF 245
Db 188 LDFRVDRSDGVAICRVDSHESNATPQVAMQVLEIHYTPSVKI---IPSTPPPGQQL 244
QY 246 ELTCEAIGKFPQPVWTVWRVDDME--POHAVLSGNPLFINNLANKTNGTYRCEASNIVGK 303
Db 245 ILACESKGLPEPLVLTWKGGLPDPDRNVSGRELNLFLNKTNGTYRCEATNTIGQ 304
QY 304 AHSYMLYVYDPTTTPPTTTTTTTTTTTTTTTTTTTTTIT 349
Db 305 SSAEYVLIVHDVENTLPLTIIIPSLTATVTTTVAITTSPTTSATTSISDNPALAGQNG 364
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QY 350 TIGAVDHAIVGGVAVVVFAEMCLILLILGRYFARHKGTYFTHKAGDAADADADATAIINA 409
Db 365 P-----DHALLGGIVAVVVVFTLCSIFLLGRLARHKGTYLTNEAKGAEDAPDADTAIINA 420
QY 420 EGGQNNSEKKEYF 423
Db 421 EGSQVNAEKKKEYF 434

Search completed: May 27, 2004, 09:34:56
Job time : 35.6885 secs
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DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro; IPR007416; P:synaptogenesis; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 235 AA; 32347 MW; FDD9B8145C6B971B CRC64;
 Query Match 68.0%; Score 1493; DB 11; Length 295;
 Best Local Similarity 96.6%; Pred. No. 2.3e-118;
 Matches 284; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 130 MIDQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELGKSEVEEWSMDYTVTSQML 189
 Db 1 MIDQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELGKSEVEEWSMDYTVTSQML 60
 QY 190 KVHKEDGVPVICOVEHPAVTGNLQRYLEVQVKPOVHIQMTYPLQGLTREGDAFELTC 249
 Db 61 KVHKEDGVPVICOVEHPAVTGNLQRYLEVQVKPOVHIQMTYPLQGLTREGDAFELTC 120
 QY 250 EAIGKPOPMVWTVRVDDEMPQHAVLSPNLFNNLNKTDNGTYRCEASNIIVGKAHSDYM 309
 Db 121 EAIGKPOPMVWTVRVDDEMPQHAVLSPNLFNNLNKTDNGTYRCEASNIIVGKAHSDYI 180
 QY 310 LYVDPPTTTPPPPTTT 369
 Db 181 LYVDPPTTTPPPPTTT 240
 QY 370 MLCLLIILGRYFARHKGTYFTHKAGDADADATAIINAEAGGNNSEKKEYF 423
 Db 241 MLCLLIILGRYFARHKGTYFTHKAGDADADATAIINAEAGGNNSEKKEYF 294
 RESULT 13
 QYQYL5
 ID QYQYL5 PRELIMINARY; PRT; 289 AA.
 AC QYQYL5;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175B.
 GN IGSF4 OR RAI175B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Uruse K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021965; BAA87915.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.

SQ SEQUENCE 289 AA; 31811 MW; 8D1B836D00565AE4 CRC64;
 Query Match 63.9%; Score 1404; DB 11; Length 289;
 Best Local Similarity 92.5%; Pred. No. 7.9e-111;
 Matches 272; Conservative 2; Mismatches 14; Indels 6; Gaps 1;
 QY 130 MIDQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELGKSEVEEWSMDYTVTSQML 189
 Db 1 MIDQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELGKSEVEEWSMDYTVTSQML 60
 QY 190 KVHKEDGVPVICOVEHPAVTGNLQRYLEVQVKPOVHIQMTYPLQGLTREGDAFELTC 249
 Db 61 KVHKEDGVPVICOVEHPAVTGNLQRYLEVQVKPOVHIQMTYPLQGLTREGDAFELTC 120
 QY 250 EAIGKPOPMVWTVRVDDEMPQHAVLSPNLFNNLNKTDNGTYRCEASNIIVGKAHSDYM 309
 Db 121 EAIGKPOPMVWTVRVDDEMPQHAVLSPNLFNNLNKTDNGTYRCEASNIIVGKAHSDYI 180
 QY 310 LYVDPPTTTPPPPTTT 369
 Db 181 LYVDPPTTTPPPPTTT 234
 QY 370 MLCLLIILGRYFARHKGTYFTHKAGDADADATAIINAEAGGNNSEKKEYF 423
 Db 235 MLCLLIILGRYFARHKGTYFTHKAGDADADATAIINAEAGGNNSEKKEYF 288
 RESULT 14
 QYQYL3
 ID QYQYL3 PRELIMINARY; PRT; 278 AA.
 AC QYQYL3;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Adhesion protein RAI175N.
 GN IGSF4 OR RAI175N.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Soyama A., Fujita E., Uruse K., Mukasa T., Kouroku Y., Momoi M.,
 RA Momoi T.;
 RT "RAI175, a novel neuron specific adhesion protein.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021967; BAA87917.1; -;
 DR MGD; MGI:1889272; Igsf4.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . .; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00294; 4.1m; 1.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;
 Query Match 62.8%; Score 1380.5; DB 11; Length 278;
 Best Local Similarity 90.8%; Pred. No. 7.4e-109;
 Matches 267; Conservative 2; Mismatches 8; Indels 17; Gaps 1;
 QY 130 MIDQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELGKSEVEEWSMDYTVTSQML 189
 Db 1 MIDQKDTAVEGEIEVNCCTAMASKPATTIRWFKGNKELGKSEVEEWSMDYTVTSQML 60
 QY 190 KVHKEDGVPVICOVEHPAVTGNLQRYLEVQVKPOVHIQMTYPLQGLTREGDAFELTC 249

QY 1 AAPPGLRLRLLLLSAALIPGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 60
 DB 22 AAPPGLRLRLLLLSAALIPGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 81
 QY 61 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSILTNVSISSDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSILTNVSISSDEGRYFCQLYTDPQESYTTI 141
 QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKNKELKKGSEVEEWSM 180
 DB 142 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKNKELKKGSEVEEWSM 201
 QY 181 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
 DB 202 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 261
 QY 241 EGDAPFELTCEAIGKQPQPMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
 DB 262 EGDAPFELTCEAIGKQPQPMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 321
 QY 301 VGKAHSDYMLVYV 313
 DB 322 VGKAHSDYMLVYV 334

RESULT 8

Q80VG4 PRELIMINARY; PRT; 336 AA.
 ID Q80VG4
 AC Q80VG4
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE A secretion form of SgIGSF/TSLC1.
 GN SgIGSF/TSLC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Spleen cell-derived;
 RA Ito A., Koma Y., Nagano T.;
 RT "A secretion form of SgIGSF/TSLC1".
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB092414; BAC66173.1; -
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IGC2; 3.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 SQ SEQUENCE 336 AA; 37155 MW; 9EF3D898BE5E8F72 CRC64;

Query Match 74.2%; Score 1631; DB 11; Length 336;
 Best Local Similarity 100.0%; Pred. No. 5.3e-130;
 Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAALIPGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 60
 DB 22 AAPPGLRLRLLLLSAALIPGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 81
 QY 61 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSILTNVSISSDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSILTNVSISSDEGRYFCQLYTDPQESYTTI 141
 QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKNKELKKGSEVEEWSM 180
 DB 142 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKNKELKKGSEVEEWSM 201
 QY 181 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
 DB 202 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 261

QY 241 EGDAPFELTCEAIGKQPQPMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
 DB 262 EGDAPFELTCEAIGKQPQPMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 321
 QY 301 VGKAHSDYMLVYV 313
 DB 322 VGKAHSDYMLVYV 334

RESULT 9

Q86WB8 PRELIMINARY; PRT; 333 AA.
 ID Q86WB8
 AC Q86WB8
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Secretory isoform of TSLC-1.
 GN TSLC-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Ito A., Koma Y., Nagano T.;
 RT "Cloning of a secretory isoform of SgIGSF/TSLC-1";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB094146; BAC66178.1; -
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 SQ SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;

Query Match 73.5%; Score 1615; DB 4; Length 333;
 Best Local Similarity 99.0%; Pred. No. 1.2e-128;
 Matches 310; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAALIPGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 60
 DB 19 AAPPGLRLRLLLLSAALIPGQNLFTKDVTVIEGEVATISCVQNKSDSDSVIQLLN 78
 QY 61 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSILTNVSISSDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNRQTIYFRDPRFLKDSRFQLLNFSSSELKVSILTNVSISSDEGRYFCQLYTDPQESYTTI 138
 QY 121 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKNKELKKGSEVEEWSM 180
 DB 139 TVLVPPRNLMIDIQKDTAVEGEIEVNCCTAMASKPATIRWFKNKELKKGSEVEEWSM 198
 QY 181 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 240
 DB 199 YTVTSQMLKVKHKEDDGVFVICOVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTR 258
 QY 241 EGDAPFELTCEAIGKQPQPMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 300
 DB 259 EGDAPFELTCEAIGKQPQPMVTVWRVDDMPQHAVLSGPNLFINNLTNDNGTYRCEASNI 318
 QY 301 VGKAHSDYMLVYV 313
 DB 319 VGKAHSDYMLVYV 331

RESULT 10

Q92ZH8 PRELIMINARY; PRT; 295 AA.
 ID Q92ZH8
 AC Q92ZH8
 DT 01-MAY-1999 (TREMBlrel. 10, Created)

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QY 161 YTVTSQMLKVKHKEDDGPVVCQVHPHVAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 240
DB 202 YTVTSQMLKVKHKEDDGPVVCQVHPHVAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 261
QY 241 EGDAPFELTCEALGKQPQVWVWVRVDDSEMPQHAVLSGNLFTNNLKNKTNGTYRCEASNI 300
DB 262 EGDAPFELTCEALGKQPQVWVWVRVDDSEMPQHAVLSGNLFTNNLKNKTNGTYRCEASNI 321
QY 301 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
DB 322 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 353
QY 361 GVVAVVVFAMLCIIILGRYPFARHKGTYFTHEAKGADDAADATTAIINAGGQNNSEKK 420
DB 354 GVVAVVVFAMLCIIILGRYPFARHKGTYFTHEAKGADDAADATTAIINAGGQNNSEKK 413
QY 421 EYF 423
DB 414 EYF 416

RESULT 6
Q8N2F4
ID Q8N2F4 PRELIMINARY; PRT; 443 AA.
AC Q8N2F4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein HEMBA1001879.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075502; BAC11657.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS0835; IG_LIKE; 3.
DR Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;

Query Match 92.0%; Score 2020.5; DB 4; Length 443;
Best Local Similarity 92.9%; Pred. No. 6.9e-163;
Matches 394; Conservative 5; Mismatches 24; Indels 1; Gaps 1;

QY 1 AAPGLRLRLLLLSAAALPTGQNLFPKQVTVIEGEVATISCVQNKSDSDSVIQLLN 60
DB 19 AAPGLRLRLLLLSAAALPTGQNLFPKQVTVIEGEVATISCVQNKSDSDSVIQLLN 78
QY 61 PNQTIYFRDPRPLKDSRFQQLNFSSELKSVLTNVSISDEGRYFCQLYTDPPOESYTTI 120
DB 79 PNQTIYFRDPRPLKDSRFQQLNFSSELKSVLTNVSISDEGRYFCQLYTDPPOESYTTI 138
QY 121 TVLVPPNLMIDIQDQTAVEGEIEVNCTAMASKPATIRFWKGNKELGKSEVEESDM 180
DB 139 TVLVPPNLMIDIQDQTAVEGEIEVNCTAMASKPATIRFWKGNKELGKSEVEESDM 198
QY 181 YTVTSQMLKVKHKEDDGPVVCQVHPHVAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 240
DB 199 YTVTSQMLKVKHKEDDGPVVCQVHPHVAVTGNLQRYLEVQKQVHIQMTYPLQGLTR 258
QY 241 EGDAPFELTCEALGKQPQVWVWVRVDDSEMPQHAVLSGNLFTNNLKNKTNGTYRCEASNI 300

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DB 239 EGDALFELTCEALGKQPQVWVWVRVDDSEMPQHAVLSGNLFTNNLKNKTNGTYRCEASNI 318
QY 301 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 359
DB 319 VGKAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378
QY 360 GVVAVVVFAMLCIIILGRYPFARHKGTYFTHEAKGADDAADATTAIINAGGQNNSEKK 419
DB 379 GVVAVVVFAMLCIIILGRYPFARHKGTYFTHEAKGADDAADATTAIINAGGQNNSEKK 438
QY 420 KEYF 423
DB 439 KEYF 442

RESULT 7
Q9D6E7
ID Q9D6E7 PRELIMINARY; PRT; 336 AA.
AC Q9D6E7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 2900073G06Rik protein.
GN IGSF4 OR 2900073G06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK013775; BAB28988.1; -.
DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0008021; C:synaptic vesicle; IDA.
DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 336 AA; 37157 MW; FF887FAF4EFDF120 CRC64;

Query Match 74.2%; Score 1631; DB 11; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.3e-130;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Query Match 99.1%; Score 2176.5; DB 11; Length 456;
 Best Local Similarity 97.2%; Pred. No. 4.1e-176;
 Matches 422; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

QY 1 AAPPGLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 DB 22 AAPPGLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 81

QY 61 PNQTIYFRDPRPLKDSRFQQLNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNQTIYFRDPRPLKDSRFQQLNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 141

QY 121 TVLVPPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
 DB 142 TVLVPPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEEWSDM 201

QY 181 YTVTSQMLKVHKEDDGVPIQVHEHFAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
 DB 202 YTVTSQMLKVHKEDDGVPIQVHEHFAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 261

QY 241 EGDAPFELTCEAIGKQPQVMVTVWRVDDDEMPQHAVLSGNFLFINLNKTNDNGTYRCEASNI 300
 DB 262 EGDAPFELTCEAIGKQPQVMVTVWRVDDDEMPQHAVLSGNFLFINLNKTNDNGTYRCEASNI 321

QY 301 VGKASHDYMLVYDDPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 349
 DB 322 VGKASHDYMLVYDDPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 381

QY 350 TIGAVDHAVIGGVAVVVFAMLCILILGRYFARHKGTYFTHKAGDAADADATAIINA 409
 DB 382 TIGAVDHAVIGGVAVVVFAMLCILILGRYFARHKGTYFTHKAGDAADADATAIINA 441

QY 410 EGGQNNSEKKEYF 423
 DB 442 EGGQNNSEKKEYF 455

RESULT 4
 Q9BY67 PRELIMINARY; PRT; 442 AA.

ID Q9BY67
 AC Q9BY67
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like protein 2.
 GN NECL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
 RT "Cloning of a novel human cDNA encoding a member of the immunoglobulin
 RT superfamily."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132811; AAF69029.1; -.
 DR Genew; HGNC:5951; IGSP4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00294; 4.1m; 1.
 DR PROSITE; PSS0835; IGLIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;

Query Match 98.6%; Score 2166; DB 4; Length 442;
 Best Local Similarity 98.6%; Pred. No. 3.1e-175;
 Matches 417; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPPGLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 DB 19 AAPPGLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 78

QY 61 PNQTIYFRDPRPLKDSRFQQLNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
 DB 79 PNQTIYFRDPRPLKDSRFQQLNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 138

QY 121 TVLVPPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
 DB 139 TVLVPPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEEWSDM 198

QY 181 YTVTSQMLKVHKEDDGVPIQVHEHFAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 240
 DB 199 YTVTSQMLKVHKEDDGVPIQVHEHFAVTGNLQRYLEVQYKPOVHIQMTYPLQGLTR 258

QY 241 EGDAPFELTCEAIGKQPQVMVTVWRVDDDEMPQHAVLSGNFLFINLNKTNDNGTYRCEASNI 300
 DB 259 EGDAPFELTCEAIGKQPQVMVTVWRVDDDEMPQHAVLSGNFLFINLNKTNDNGTYRCEASNI 318

QY 301 VGKASHDYMLVYDDPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 360
 DB 319 VGKASHDYMLVYDDPPTIIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 378

QY 361 GVAVVVFAMLCILILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 420
 DB 379 GVAVVVFAMLCILILGRYFARHKGTYFTHKAGDAADADATAIINAEGGQNNSEKK 438

QY 421 EYF 423
 DB 439 EYF 441

RESULT 5
 Q7TNL1 PRELIMINARY; PRT; 417 AA.

ID Q7TNL1
 AC Q7TNL1
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nectin-like molecule 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S.,
 RA Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
 RT "Implications of nectin-like molecule
 RT 2/IGSF4/RA175/SGISF/TSCL1/SyncM1 in cell-cell adhesion and
 RT transmembrane protein localization in epithelial cells."
 RL J. Biol. Chem. 0:0-0(2003).
 DR EMBL; AY351388; AAQ02381.1; -.
 SQ SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;

Query Match 92.3%; Score 2027; DB 11; Length 417;
 Best Local Similarity 93.4%; Pred. No. 1.8e-163;
 Matches 395; Conservative 0; Mismatches 0; Indels 28; Gaps 1;

QY 1 AAPPGLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 60
 DB 22 AAPPGLRLRLLLLSAAALIPGTGQNLFTKDVTVIEGEVATISCVNKSDDSVIQLLN 81

QY 61 PNQTIYFRDPRPLKDSRFQQLNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 120
 DB 82 PNQTIYFRDPRPLKDSRFQQLNFSSSELKVSILNVSISDEGRYFCQLYTDPQESYTTI 141

QY 121 TVLVPPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEEWSDM 180
 DB 142 TVLVPPRLNLMIDIQKDTAVEGEIEIVNCTAMASKPATIRWFKGNKELKGKSEVEEWSDM 201

Matches	423;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	AAPEGLRLRLILLLSAAALPTGDGNLFKDVTVIEGEVATISCVQNKSDSDSVIQLLN	60						
Db	22	AAPGLRLRLILLLSAAALPTGDGNLFKDVTVIEGEVATISCVQNKSDSDSVIQLLN	81						
Qy	61	PNRQTIYFRDPRFLKDSRPOLLNPFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESYTTI	120						
Db	82	PNRQTIYFRDPRFLKDSRPOLLNPFSSSELKVSILTNVSIISDEGRYFCQLYTDPQESYTTI	141						
Qy	121	TVLVPPRNLMIDIQKQTA VGEELVNTAWASKPATIRWFKGNKELKKGSEVEBWSDM	180						
Db	142	TVLVPPRNLMIDIQKQTA VGEELVNTAWASKPATIRWFKGNKELKKGSEVEBWSDM	201						
Qy	181	YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTORYLEVQYKPVQVHIQMTYPLQGLTR	240						
Db	202	YTVTSQMLKVHKEDDGPVVCQVEHPAVTGNLQTORYLEVQYKPVQVHIQMTYPLQGLTR	261						
Qy	241	EGDAFELTCEAIGKPPQPMVTVRVDDMPQHAVLGSPLFINLNKNTDNGTYVRCASNI	300						
Db	262	EGDAFELTCEAIGKPPQPMVTVRVDDMPQHAVLGSPLFINLNKNTDNGTYVRCASNI	321						
Qy	301	VGAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTITITDTSRAGEEGTIGAVDHA	360						
Db	322	VGAHSDYMLVYVDPPTTIPPTTTTTTTTTTTTTTTTTTTTTTTITITDTSRAGEEGTIGAVDHA	381						
Qy	361	GVAVVVFVFMCLLIILGRYFARHKGTYFTHEAKGADDAADADATAIINAEAGGQNNSEKK	420						
Db	382	GVAVVVFVFMCLLIILGRYFARHKGTYFTHEAKGADDAADADATAIINAEAGGQNNSEKK	441						
Qy	421	EYF 423							
Db	442	EYF 444							

RESULT 2

Q8K3T6

ID Q8K3T6 PRELIMINARY; PRT; 445 AA.

AC Q8K3T6;

DT 01-OCT-2002 (TEMBLrel. 22, Created)

DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TEMBLrel. 25, Last annotation update)

DE Synaptic cell adhesion molecule 1.

GN IGSP4

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID:10090;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL;

RC Biedler T.C.;

RA Sudhof T.C.;

RT "syncam, a synaptic adhesion molecule that drives synapse assembly.";

RL Science 0:0-0(2002).

DR EMBL; AF539424; AAN01614.1; -.

DR MGD; MGI:1899272; Igsf4.

DR GO; GO:0045202; C:synaptic junction; IDA.

DR GO; GO:0008021; C:synaptic vesicle; IDA.

DR GO; GO:0016347; F:calcium-independent cell adhesion molecule . . ; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR GO; GO:0007416; P:synaptogenesis; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PF00047; Ig_3.

DR SMART; SM00409; IG; 3.

DR SMART; SM00408; IGC2; 3.

DR PROSITE; PS50835; IG_LIKE; 3.

DR Immunoglobulin domain.

SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match	99.8%;	Score 2193;	DB 11;	Length 445;																																																		
Best Local Similarity	99.8%;	Pred. No. 1.6e-177;																																																				
Matches 422;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;																																																		
QY	1	AAPGLRLRLLLLLL	SAALIP	TG	QGNLF	KDV	TV	IE	GE	VATIS	CO	VN	KS	DD	S	V	I	Q	L	L	N	60																																
Db	22	AAPGLRLRLLLLLL	SAALIP	TG	QGNLF	KDV	TV	IE	GE	VATIS	CO	VN	KS	DD	S	V	I	Q	L	L	N	81																																
QY	61	PNROTIVPRD	PR	PL	KDS	R	FL	N	SS	S	SEL	K	V	S	L	T	N	V	S	I	S	DE	GR	Y	F	C	Q	L	Y	T	D	P	P	Q	S	Y	T	I	120															
Db	82	PNROTIVPRD	PR	PL	KDS	R	FL	N	SS	S	SEL	K	V	S	L	T	N	V	S	I	S	DE	GR	Y	F	C	Q	L	Y	T	D	P	P	Q	S	Y	T	I	141															
QY	121	TVLVPPNLM	I	D	I	O	K	T	A	V	E	E	E	E	V	N	T	A	M	A	S	K	P	A	T	T	I	R	P	F	G	K	N	K	E	L	G	K	E	V	E	W	S	D	M	180								
Db	142	TVLVPPNLM	I	D	I	O	K	T	A	V	E	E	E	E	V	N	T	A	M	A	S	K	P	A	T	T	I	R	P	F	G	K	N	K	E	L	G	K	E	V	E	W	S	D	M	201								
QY	181	YTVTSQ	L	M	L	K	V	H	K	E	D	D	G	V	P	V	I	C	Q	V	E	H	P	A	T	G	N	L	O	R	Y	L	E	V	Q	Y	K	P	Q	V	H	I	O	M	T	Y	P	L	Q	G	L	T	R	240
Db	202	YTVTSQ	L	M	L	K	V	H	K	E	D	D	G	V	P	V	I	C	Q	V	E	H	P	A	T	G	N	L	O	R	Y	L	E	V	Q	Y	K	P	Q	V	H	I	O	M	T	Y	P	L	Q	G	L	T	R	261
QY	241	EGDAFELT	C	E	A	I	G	K	P	Q	P	P	V	M	T	W	R	V	D	D	E	M	P	O	H	A	V	L	S	G	N	L	F	I	N	N	L	K	T	D	N	G	T	Y	R	C	E	A	S	N	I	300		
Db	262	EGDAFELT	C	E	A	I	G	K	P	Q	P	P	V	M	T	W	R	V	D	D	E	M	P	O	H	A	V	L	S	G	N	L	F	I	N	N	L	K	T	D	N	G	T	Y	R	C	E	A	S	N	I	321		
QY	301	VGKAHSD	Y	M	L	K	V	Y	D	P	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	360				
Db	322	VGKAHSD	Y	M	L	K	V	Y	D	P	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	381				
QY	361	GVAVVVF	F	A	M	L	C	L	L	I	L	G	R	Y	F	A	R	H	K	G	T	F	T	H	E	A	K	G	A	D	A	A	D	A	T	I	N	A	E	G	Q	N	N	S	E	E	K	420						
Db	382	GVAVVVF	F	A	M	L																																																

DR	GO: 0016347; F-actin-binding; actin.
DR	GO: 0016347; F-actin-independent cell adhesion molecule . . ; IDA.
DR	GO: 0000515; F-protein binding; IPI.
DR	GO: 0000715; P-cell adhesion; IDA.
DR	GO: 0007416; P-synaptogenesis; IDA.
DR	InterPro: IPR007110; Ig-like.
DR	InterPro: IPR003598; Ig_c2.
DR	InterPro: IPR003585; Neurexin-like.
DR	Ffam; PF00047; ig; 3.
DR	SMART; SM00294; 4.1m; 1.
DR	SMART; SM00408; IGC2; 1.
DR	PROSITE; PS50835; IG_LIKE; 3.
KW	Immunoglobulin domain.
SQ	SEQUENCE 456 AA; 49787 MW; 3236E866A4BC1C7F CRC64;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 34.6885 Seconds

(without alignments)
3847.506 Million cell updates/sec

Title: US-09-778-187B-4

Perfect score: 2197

Sequence: 1 AAPGLRLRLILLLSAAL.....TAIINAEQQNSSEKKEKF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_muc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2197	100.0	445	11 Q8R4L1	Q8R4L1 mus musculus
2	2193	99.8	445	11 Q8K3T6	Q8K3T6 mus musculus
3	2176.5	99.1	456	11 Q8B5M8	Q8B5M8 mus musculus
4	2166	98.6	442	4 Q8B67	Q8B67 mus musculus
5	2027	92.3	417	11 Q7TNL1	Q7TNL1 mus musculus
6	2020.5	92.0	443	4 Q8N2F4	Q8N2F4 mus musculus
7	1631	74.2	336	11 Q9D6E7	Q9D6E7 mus musculus
8	1631	74.2	336	11 Q80VG4	Q80VG4 mus musculus
9	1615	73.5	333	4 Q86WB8	Q86WB8 mus musculus
10	1545	70.4	295	11 Q922H8	Q922H8 mus musculus
11	1513.5	68.9	306	11 Q9QYL4	Q9QYL4 mus musculus
12	1493	68.0	295	11 Q9QYL6	Q9QYL6 mus musculus
13	1404	63.9	289	11 Q9QYL5	Q9QYL5 mus musculus
14	1380.5	62.8	278	11 Q9QYL3	Q9QYL3 mus musculus
15	897	40.8	435	4 Q8N3J6	Q8N3J6 mus musculus
16	895	40.7	437	4 Q81ZP8	Q81ZP8 mus musculus

17	864	39.3	404	11 Q8BLQ9	Q8BLQ9 mus musculus
18	860	39.1	404	11 Q8BYP1	Q8BYP1 mus musculus
19	857	39.0	395	11 Q8BXJ7	Q8BXJ7 mus musculus
20	854	38.9	395	11 Q8B2P4	Q8B2P4 mus musculus
21	800	36.4	394	13 Q7ZXX1	Q7ZXX1 xenopus lae
22	766.5	34.9	388	4 Q8NFZ8	Q8NFZ8 mus musculus
23	757.5	34.5	388	11 Q8R464	Q8R464 mus musculus
24	739.5	33.7	396	11 Q9N28	Q9N28 mus musculus
25	732.5	33.3	398	4 Q8N126	Q8N126 mus musculus
26	730.5	33.2	381	4 Q9Y4A4	Q9Y4A4 mus musculus
27	715.5	32.6	432	4 Q9UJF1	Q9UJF1 mus musculus
28	371.5	16.9	163	11 Q8KIH8	Q8KIH8 mus musculus
29	362.5	16.5	163	4 Q9NVJ5	Q9NVJ5 mus musculus
30	360.5	16.4	152	11 Q8BSQ8	Q8BSQ8 mus musculus
31	337.5	15.4	549	11 Q9D006	Q9D006 mus musculus
32	334.5	15.2	549	11 Q9JLB9	Q9JLB9 mus musculus
33	325.5	14.8	549	4 Q9NQS3	Q9NQS3 mus musculus
34	323	14.7	234	4 Q81ZQ9	Q81ZQ9 mus musculus
35	303.5	13.8	438	11 Q9JLB7	Q9JLB7 mus musculus
36	303.5	13.8	510	11 Q9JLB8	Q9JLB8 mus musculus
37	283	12.9	439	13 Q57349	Q57349 gallus gall
38	270	12.3	407	4 Q9Y412	Q9Y412 mus musculus
39	263	12.0	1482	5 Q9V4Y0	Q9V4Y0 drosophila
40	261.5	11.9	5175	5 Q810L3	Q810L3 caenorhabdi
41	261.5	11.9	5198	5 Q76518	Q76518 caenorhabdi
42	248.5	11.3	624	11 Q8CIJ4	Q8CIJ4 mus musculus
43	248.5	11.3	789	11 Q80W68	Q80W68 mus musculus
44	247.5	11.3	467	11 Q91VT9	Q91VT9 mus musculus
45	247.5	11.3	510	4 Q96NY8	Q96NY8 mus musculus

ALIGNMENTS

RESULT 1

Q8R4L1	Q8R4L1	PRELIMINARY;	PRT;	445 AA.
ID	Q8R4L1			
AC	Q8R4L1			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, last annotation update)			
DE	Tumor suppressor in lung cancer 1.			
GN	IGSF4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129/SvJ;			
RA	Fukami T., Maruyama T., Murakami Y.;			
RT	Identification of murine orthologue of the TSLC1 gene.;			
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF434663; AAL86736.1; -			
DR	MGD; MGI:1889272; Igsf4.			
DR	GO; GO:0045202; C:synaptic junction; IDA.			
DR	GO; GO:0008021; C:synaptic vesicle; IDA.			
DR	GO; GO:0016347; F:calcium-independent cell adhesion molecule . . . ; IDA.			
DR	GO; GO:0005515; F:protein binding; IPI.			
DR	GO; GO:0007155; P:cell adhesion; IDA.			
DR	GO; GO:0007416; P:synaptogenesis; IDA.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003598; Ig_c2.			
DR	InterPro; IPR003585; Neurexin-like.			
DR	Pfam; PF00047; ig; 3.			
DR	SMART; SM00294; 4.1m; 1.			
DR	SMART; SM00408; IGC2; 1.			
DR	PROSITE; PS50835; IG_LIKE; 3.			
KW	Immunoglobulin domain.			
SQ	SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;			
Query Match	100.0%;	Score 2197;	DB 11;	Length 445;
Best Local Similarity	100.0%;	Pred. No. 7.3e-178;		


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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PS50835; Ig LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1092
FT
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT TRANSMEM 724 1092
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 208 295
FT DOMAIN 303 397
FT DOMAIN 400 489
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
FT CARBOHYD 341 341
FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
SQ SEQUENCE 1092 AA; 118082 MW; CD236E0E9F8B7AD1 CRC64;

Query Match 10.1%; Score 222; DB 1; Length 1092;
Best Local Similarity 23.9%; Pred. No. 2.9e-08;
Matches 81; Conservative 68; Mismatches 150; Indels 40; Gaps 15;

QY 32 KDVTVEIEGAVTISC---QVKS---DVSQVLN-----PQRQIYFRDFPLKDSRFQL 81
Db 199 KDIQIVNVPLPQARQIRVATNANMDSVLSCDADGFPDPFISWLKKGSPIDEGE-EK 257
QY 82 LNFSSSELKSLTNVSIISDEGRYFCQLYDPPQBSYTTITVLVPPRNLMDIQKDTAVEG 141
Db 258 ISFNEDKSEMTIYRVEKEDEAEYSC-IANNOAGEAEAILVKVAKPKMTYVKNKTVEL 316
QY 142 BEIEVNCAMASKPATITIRWFKGNKELKGSKEVSEWSDMYTWT-----SQMLKVKHED 195
Db 317 DEITLTCEA-SCDPTPSITWRTAHRNI---SSEKTLDGHIWVKDHIRMSALTLDIQYT 372
QY 196 DGVPIQVQHPAVTGNLTQRYLEVQYKPVHIQMTYPLQGLTFREGDAFELTCEATGKP 255
Db 373 DAGEYFCVASNP-IGVDQAM-YFEVQAPKIR---GPVVVYWEQNPVNITCDVLAHP 426
QY 256 QPVMVTVVRVDEMPQH-----AVLSGP---NLFINLNKTDNGYRCEASNVGKAHSD 307
Db 427 S-AAVSWEFDQLLPSSNFSNFKIYNGTFFSLEVPDSEDFGNYCSAVNSIGHESSE 485
QY 308 YMLVYVDPPTPIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
Db 486 FILVQADTPSS---PAIRKVPYPSVSTVMVDFEPPDATGG 521

RESULT 15
ID NPHN MOUSE
AC Q9QZS7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
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10-OCT-2003 (Rel. 42, Last annotation update)
Nephlin precursor (Renal glomerulus-specific cell adhesion receptor).
NPHS1 OR NPHN
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1] NCBI_TaxID=10090;
SEQUENCE FROM N.A. AND SUBCELLULAR LOCATION.
MEDLINE=99436348; PubMed=10504499;
Holzman L.B., St John P.L., Kovari I.A., Verma R., Holthofer H.,
Abramson D.R.;
"Nephlin localizes to the slit pore of the glomerular epithelial
cell.";
Kidney Int. 56:1481-1491(1999).
[2]
INTERACTION WITH CD2AP.
MEDLINE=21590051; PubMed=11733379;
Shih N.Y., Li J., Cotran R., Mundel P., Miner J.H., Shaw A.S.;
"CD2AP localizes to the slit diaphragm and binds to nephrin via a
novel C-terminal domain.";
Am. J. Pathol. 159:2303-2308(2001).
[3]
INTERACTION WITH CD2AP AND NPHS2.
MEDLINE=21590460; PubMed=11733557;
Schwarz K., Simons M., Reiser J., Saleem M.A., Paul C., Kriz W.,
Shaw A.S., Holzman L.B., Mundel P.;
"Podocin, a raft-associated component of the glomerular slit
diaphragm, interacts with CD2AP and nephrin.";
J. Clin. Invest. 108:1621-1629(2001).
-!- FUNCTION: Seems to play a role in the development or function of
the kidney glomerular filtration barrier. May anchor the podocyte
slit diaphragm to the actin cytoskeleton.
-!- SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
domain.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Located
at podocyte slit diaphragm between podocyte foot processes.
-!- TISSUE SPECIFICITY: Expressed in kidney glomeruli.
-!- PM: Phosphorylated on tyrosine residues (By similarity).
-!- SIMILARITY: Belongs to the immunoglobulin superfamily.
-!- SIMILARITY: Contains 8 immunoglobulin-like domains.
-!- SIMILARITY: Contains 1 fibronectin type III domain.

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or send an email to license@isb-sib.ch).

EMBL; AF168466; AAF03368.1; -;
MGD; MGI:1859637; Nphs1.
GO; GO:0005515; P:Protein binding; IPI.
GO; GO:0007254; P:JNK cascade; IDA.
GO; GO:0000165; P:MAPKKK cascade; IDA.
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 1.
Pfam; PF00047; ig; 8.
SMART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 8.
Cell adhesion; Transmembrane; Signal; Glycoprotein;
Immunoglobulin domain; Repeat; Phosphorylation.
FT SIGNAL 1 22
FT CHAIN 23 1242
FT DOMAIN 23 1064
FT TRANSMEM 1065 1086
FT DOMAIN 1087 1242
FT DOMAIN 130
IG-LIKE C2-TYPE 1.

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164 QY      -TSQLMLKVHREDDGPVICQVEHPAVTGNLQTORXLYLEVQYKPQVHIQMTYPLQGLTREG 242
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
262 Db      SNTETVNRNINISDGGPVCVRATNKA--GEDEKQAFLOQVFOQPHI-IOLK---NETTYEN 315
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
243 QY      DAFELTCRAIGKQPQPMVWTVVR-VD-----DEMP-----QHAVLSGPNLFINNLN 286
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
316 Db      GQVTLVCDAGEPIP-EITWKRVDGFTFTGDKSPDGRIEVKGQH---GSSSLHIKDVK 371
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
287 QY      KTDNGTYRCE-ASNIIVGAHSDYMLYYI-----
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
372 Db      LSGSGRYDCEAASRIGGHQKSMYLDIYAPKFIISNOTIYYSWEGNPINISCDVKSNPPAS 431
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
319 QY      I-----PPPTTTTTTTTTTTTTTTTTLITITSRAGEEGTICADVHNAVIGGVAVVVEFA 369
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432 Db      IHWRRDKLVLPKATNTNLKTYSTGRKMILEIAPTSNDNDFGRYNCTATNHIGTRFQBYILA 491
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370 QY      MLCL-----LIILGRFYAR-----HKGYTFTHAEAKGADDAADADTAIINAEQGQ 413
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
492 Db      LADVPSSPYGVKTIELSOTTAKVSNFKPDSHGGVPPIHYQVDVKEVASEIWKIVSRHGVQ 551
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414 QY      -----NNSEEKEY 422
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552 Db      TMVLNNLEPNNTY 565
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RESULT 14
NCA2_XENLA
ID   NCA2_XENLA      STANDARD;          PRT;  1092 AA.
AC   P36335;
CD
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
DE   180).
DE   NCAM2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxId=8335;
RN   [1]
RP   SEQUENCE FROM N.A.
RP   MEDLINE=93273239; PubMed=7684721;
RT   Tonissen K.F., Krieg P.A.;
RT   "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
RT   laevis are expressed during development and in adult tissues.";
RL   Gene 127:243-247(1993).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC   neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC   neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=1;
CC   Comment=A number of isoforms are produced;
CC   Name=1;
CC   IsoId=P36335-1; Sequence=displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
CC   at the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announcement
CC   or send an email to license@isb-sib.ch).
CC
CC   EMBL; M76710; AAA49910.1; -.
CC   F01931; J06635; J06635.
CC   HSP; P56276; 1ILK.
CC   InterPro; IPR008957; FN III-like.
CC   InterPro; IPR003961; FN III.

```

RX MEDLINE=97369238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
RT related to zone-to-zone projection of olfactory and vomeronasal
RT axons.";
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
RT with a potential role in selective axonal projection.";
RL J. Biol. Chem. 272:26083-26086(1997).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=035136-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=035136-2; Sequence=VSP 002590;
CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
CC vomeronasal neurons in a zone-specific manner.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AF001287; AAB69125.1; -;
DR EMBL; AF001286; AAB69124.1; -;
DR EMBL; AF016619; AAC53375.1; -;
DR MGD; MGI:97282; NCAM2
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00835; IG LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT SIGNAL 1 19
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FT DOMAIN 20 697
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FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 321 321 GPI-anchor amidated asparagine
(POTENTIAL).
SQ SEQUENCE 344 AA; 37998 MW; CBB39BES3H3B224 CRC64;

Query Match 10.5%; Score 231; DB 1; Length 344;
Best Local Similarity 26.2%; Pred. No. 1.5e-09;
Matches 85; Conservative 56; Mismatches 134; Indels 50; Gaps 15;

QY 10 LLLLLLSAALIPTG-----DQNLFTK---DVTVIEGEVATISQVNVKSDSVIQLNPN 62
Db 14 LVVSLRLFLVPTGVPVRSQDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAWLN 70
QY 63 RQTI-YFRDFRPLKDSRFQLLNFSSSELKVLNVSISDEGRYFCQLYTD-PPQESYTTI 120
Db 71 RSTILYAGNDKWCLDPRVLLSNTQTSYIEIQNVVDVDEGPTCSQTDNHPKTSRVHL 130
QY 121 TVLVPPRLMIDIQKTAV-EGEIEVNCVTAMASKPATIRWFKGNKELGKSEVEWSD 179
Db 131 IVQVSPK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTRHISPKAVGFVSEDEYLE 187
QY 180 MYTVTSQMLKLVH---KEDDGVPIQVEHPAVTGNLQTORYLEVQYKPVQHIQMTYPLQ 236
Db 188 IQGITREQSGDEYCSASNDVAAPVVRV-----VTNYPYVIS-----EAK 229
QY 237 GL-TREGDAFELTCEATGKQFVMTVVRVDEMPQ-----HAVLSGNLFINLN 286
Db 230 GTGVPVQKGTQCEASAVPS-AEFQWFKDKRLVEGKGVKVENRFLSLRFTF---NVS 286
QY 287 KTNGTYRCEASNIIVGKAHSDYMLY 311
Db 287 EHDYGNVTCVASKLGHNTASIMLF 311

RESULT 11
NTRI HUMAN
ID NTRI HUMAN STANDARD; PRT; 344 AA.
AC Q9P121;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor (hNT).
GN NT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
RT *Cloning and identification of human neurotrophin full length cDNA.*;
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLN
family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF126426; AAF37591.1; -.
DR MIM; 607938; -.
DR GO; GO:0008038; P:neuronal cell recognition; TAS.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS00835; Ig_Like; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
Repeat; Signal; Lipoprotein.
FT CHAIN 1 31 POTENTIAL.
FT SIGNAL 32 321 NEUTROTRIN.
FT PROPEP 322 344 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 126 IG-LIKE C2-TYPE 1.
FT DOMAIN 136 218 IG-LIKE C2-TYPE 2.
FT DOMAIN 222 309 IG-LIKE C2-TYPE 3.
FT DISULFID 57 115 POTENTIAL.
FT DISULFID 157 201 POTENTIAL.
FT DISULFID 243 295 POTENTIAL.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 321 321 GPI-anchor amidated asparagine
(POTENTIAL).
SQ SEQUENCE 344 AA; 37971 MW; DA4D12C295ABBE3A CRC64;

Query Match 10.4%; Score 229; DB 1; Length 344;
Best Local Similarity 26.3%; Pred. No. 2.1e-09;
Matches 85; Conservative 57; Mismatches 135; Indels 46; Gaps 15;

QY 10 LLLLLLSAALIPTG-----DQNLFTK---DVTVIEGEVATISQVNVKSDSVIQLNPN 62
Db 14 LVVSLRLFLVPTGVPVRSQDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAWLN 70
QY 63 RQTI-YFRDFRPLKDSRFQLLNFSSSELKVLNVSISDEGRYFCQLYTD-PPQESYTTI 120
Db 71 RSTILYAGNDKWCLDPRVLLSNTQTSYIEIQNVVDVDEGPTCSQTDNHPKTSRVHL 130
QY 121 TVLVPPRLMIDIQKTAV-EGEIEVNCVTAMASKPATIRWFKGNKELGKSEVEWSD 179
Db 131 IVQVSPK--IVEISSDISINEGNNISLTCTA-TGRPEPTVTRHISPKAVGFVSEDEYLE 187
QY 180 MYTVTSQMLKLVH---KEDDGVPIQVEHPAVTGNLQTORYLEVQYKPVQHIQMTYPLQ 236
Db 188 IQGITREQSGDEYCSASNDVAAPVVRV-----VTNYPYVIS-----EAK 229
QY 237 GL-TREGDAFELTCEATGKQFVMTVVRVDEMPQ-----AVLSGP---NLFNNLTKT 288
Db 230 GTGVPVQKGTQCEASAVPS-AEFQWFKDKRLIEGKGVKVENRFLSKLIFNVSEH 288
QY 289 DNGTYRCEASNIIVGKAHSDYMLY 311
Db 289 DYGNVTCVASKLGHNTASIMLF 311

RESULT 12
NCM2 MOUSE
ID NCM2 MOUSE STANDARD; PRT; 837 AA.
AC Q35136; Q35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;

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DR PIR; A43024; RWHUPD.
DR PIR; S12048; RWHUPA.
DR Genew; HGNC:9705; PVR.
DR MIM; 173850; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007125; F:invasive growth; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig_3.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 1 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VARSPPLIC 340 384
FT VARSPPLIC 331 331
FT VARSPPLIC 332 384
FT VARSPPLIC 385 392
FT VARSPPLIC 393 417
FT VARIANT 67 67
FT VARIANT 340 340
FT SEQUENCE 417 AA; 45302 MW; D15C012C853169B CRC64;

Query Match 10.5%; Score 231.5; DB 1; Length 417;
Best Local Similarity 25.3%; Pred. No. 1.8e-09;
Matches 101; Conservative 53; Mismatches 174; Indels 71; Gaps 16;

Qy 10 LLLLLLSAALIPGDGNLFKDVTV-----IGEVATISQV---NKSDSDVIQL 58
Dy 11 LLLVALLVLSWPPPGTG-----DVVQAPQVQFGLGDSVTLFCYLQVNMVTHVSQ 64

Qy 59 L-----NPNRQTYFRDFRPLKDSRFQLNFSSELKSLTVNS-----ISDSGRYFCQ 107
Dy 65 TWARHGSGSMNVPHQTQPGSYRSKSLFVFAARLGAELRNASLRFGLRVEDSGNYTC- 123

Qy 108 LYTPDPQSYTT---ITVLVPRNLMIDIQKDTAVEGEIEV-NCTAMASKPATIRWFK 163
Dy 124 LFVTFPQGSRSVDIWLRLAKPON-TAEVQK-VOLTGPVPMARCVSTGGRPQAIIWHS 181

Qy 164 GNKLKKGSEVEEW-SDMYTYSQLMLKVHEDDGVPVICQVEHPATVGNLQTORYLEVQ 222
Dy 182 DLGMNPTSQVFGSLGTVTVTSWLIVPSSQVQDKNVTCKVESFEKPOLLTNLTIV 241

Qy 223 YKQVHIQMTYPLQGLTREGDAFELTCEAIKCPQPMVMVTVRVDDMPQHAVLSGNLFI 282
Dy 223 YKQVHIQMTYPLQGLTREGDAFELTCEAIKCPQPMVMVTVRVDDMPQHAVLSGNLFI 282
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KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 1088
FT
FT DOMAIN 20 705
FT TRANSMEM 706 723
FT DOMAIN 724 1088
FT DOMAIN 20 108
FT DOMAIN 113 202
FT DOMAIN 209 294
FT DOMAIN 303 397
FT DOMAIN 400 484
FT DOMAIN 512 589
FT DOMAIN 618 686
FT DOMAIN 149 153
FT DOMAIN 158 162
FT DISULFID 41 93
FT DISULFID 136 186
FT DISULFID 232 282
FT DISULFID 323 379
FT DISULFID 420 473
FT CARBOHYD 82 82
FT CARBOHYD 219 219
FT CARBOHYD 310 310
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FT CARBOHYD 417 417
FT CARBOHYD 443 443
FT CARBOHYD 472 472
FT VARSPLIC 804 1049
FT
SQ SEQUENCE 1088 AA; 11778 MW; 6273855B03F3E83 CRC64;

Query Match 10.7%; Score 234; DB 1; Length 1088;
Best Local Similarity 25.9%; Pred. No. 3.9e-09;
Matches 88; Conservative 62; Mismatches 148; Indels 42; Gaps 15;

QY 32 KDVTIVIEGATISC---QVKNK---DDSVQLN-----PNQTIYFRDPLKDSRFL 81
DB 199 KDQIVNVPTIQARQLRVNATANAESVLSDCADGDFDPEISWLKGEIPBDGE-EK 257
QY 82 LNFSSSELKSLTVNVSIDSEGRYPCQLYTPQPSRYTTITVLVPRNLMDIQKDTAVEG 141
DB 258 ISFNDQSEMTIHKVEXDDEAEYSC-TANNAGAEATILLKVAKPKIYVENKTAVEL 316
QY 142 BEIEVNTAMASKPATIRWPKGNK-----LKGKSEVEESDMYTVTSQMLKVHKE 194
DB 317 DEILTCEA-SGDPIPSITWRTAVRNISSEATTLDDGHVVKHEIRM-----SALTLDKI 371
QY 195 DGGVPIVQVHEPVTGNLQTVLEQYKPOVHIQMTYPLQGLTRGDAFELTCEALGK 254
DB 372 TDAGEYFCIASNP-IGVDMQAM-YFEQVAPKIR-----GPVVVTVWGNPNVITCEVFAH 425
QY 255 PQPVMTVWRVDDMPQH-----AVLSGP-----NLFINNKLTDNGTYRCEASNIVGKAHS 306
DB 426 PR-AAVTFWRDGLQLPSSNFENIKIYSGPTSSLEVNPDSNDFGNYNCTAINIGHEFS 484
QY 307 DYMLYVVDPTTIPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 346
DB 485 EFILVQADTPSS---PAIRKVEPYSSTVMIVDFDPDSTGG 521

RESULT 8
NTRI_MOUSE STANDARD; PRT; 344 AA.
AC Q99PJ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurotrophin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

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SEQUENCE FROM N.A.
 STRAIN=ICR; TISSUE=Brain;
 Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
 "Cloning and expression of mouse neurotrophin gene in the developing nervous system.";
 Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.
 STRAIN=C57BL/6; TISSUE=Eye;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Neural cell adhesion molecule.
 -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON family.

-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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EMBL; AF282980; AA00276.1; -
 EMBL; BC023307; AA023307.1; -
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003599; Ig.
 InterPro; IPR003598; Ig_c2.
 Pfam; PF00047; Ig; 3.
 SMART; SMC0409; IG; 3.
 SMART; SMC0408; IGC2; 3.
 PROSITE; PS50835; IG LIKE; 3.
 Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
 Repeat; Signal; Lipoprotein.
 SIGNAL 1 31 POTENTIAL.
 CHAIN 32 321 NEUTROTRIMIN.
 PROPEP 322 344 REMOVED IN MATURE FORM (POTENTIAL).
 DOMAIN 39 126 IG-LIKE C2-TYPE 1.
 DOMAIN 136 218 IG-LIKE C2-TYPE 2.
 DOMAIN 222 309 IG-LIKE C2-TYPE 3.
 DISULFID 57 115 POTENTIAL.
 DISULFID 157 201 POTENTIAL.
 DISULFID 243 295 POTENTIAL.
 CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 305 305 N-LINKED (GLCNAC. .) (POTENTIAL).
 CARBOHYD 321 321 N-LINKED (GLCNAC. .) (POTENTIAL).
 LIPID 321 321 GPI-anchor amidated asparagine


```

RL J. Virol. 73:4493-4497(1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY
CC INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M80206; AA319734.1; -
CC EMBL; D26107; BA051031.1; -
CC EMBL; BC059941; AA59941.1; -
CC PIR; A38211; HLMSP3.
CC PIR; A53437; A53437.
CC MGI; MGI:97822; Pvr12.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 3.
CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
CC Repeat; Alternative splicing.
CC SIGNAL 1 31
CC CHAIN 32 530
CC DOMAIN 32 351
CC TRANSMEM 352 372
CC DOMAIN 373 530
CC DOMAIN 372 147
CC DOMAIN 153 247
CC DOMAIN 252 337
CC DISULFID 54 131
CC DISULFID 174 229
CC DISULFID 274 320
CC CARBOHYD 128 138
CC CARBOHYD 138 138
CC CARBOHYD 315 315
CC VARSPLIC 339 467
CC -----
CC ORLAADAEELGPPSYKPTKAKLEPEMPQLFTGA
CC SEHSPVTKPTFDAGVSCADQEMPRYHELPTELEERSGLLGG
CC ATGLGP -> DTPQASRDVGLVAVGGLVLLAGGL
CC ALILRGERRRKSFGGCGNDGDSYDPTQVFGNGGFVFW
CC RSASPENRPRGDEEEEMKAEGLMPPHESPRODM
CC ESHDGLSLISRAVYV (in isoform Alpha).
CC /Fttid=VSP_002630.
CC Missing (in isoform Alpha).
CC /Fttid=VSP_002631.
CC SEQUENCE 530 AA; 57317 MW; 0ED71BF0B231B9E CRC64;
CC -----
Query Match 11.1%; Score 243; DB 1; Length 530;
Best Local Similarity 22.6%; Pred. No. 3.5e-10;
Matches 90; Conservative 61; Mismatches 162; Indels 86; Gaps 14;
CC 4 PGLRLRLLLLSAAALPTGDGNLFTKQVTVIEGV--ATISQCV----- 48
CC 14 PTLPLLELLLL-----LQETG-ADQVRVLFVVRGLGTGVLPCHLLPPTTVERVSQVT 68
CC 49 -NKSDSDSVIQLLNPRTQITFRDRFRLKDSRFQI-----LNFSSELKVSILTVNIS 99
CC 69 WORLDGTWAAFHPS----FGVDPFNSQFSKDRLSFVRAPETNADLRLATLAPRGURVE 124

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QY 100 DEGRYFCOLYDTP--POESYTTITVLVPPRNLMDIOKDTAVEGEIEV-----NCT 149
DQ 125 DEGNYTCEFATFPNGTRRGVTLWRVIAQPN-----HAEAEVITIGPSVAARCV 175
QY 150 AMASKPATIRWFKG-NKELKKGKSEVEEWSMDYVTSQLMLKVHKEDDGVPIQVHEHPA 208
DQ 176 STGGRPPARITWISSLGEAKDQEPGIAQGTVTIIISKYSLVFVGRADGVKVTCKRVEHES 235
QY 209 VTGNLQRYLEVQYKPVHQMITYPLQGLTREGDAFELTCEALGKQPVVMVTVVRVDDE 268
DQ 236 FEEPIILLPVTLVSRYPPPEVSI-S-GYDDNWYLGRSEAI-LTCDVRSNPEPTDYDNSTISGV 293
QY 269 MPQHAVLSGPNLFNNLNKTDNGTYRCEASNIYKHAHSDYMLYVYDPTTTPPTTTTTT 328
DQ 294 PPASAVAQGSOLLVHSDVMVNTTFTCTNAVGTGRAEQVILVRESFST----- 343
QY 329 TTTTTLTITITDSRAGEECTIGAVDHAVIGGVAVVW 367
DQ 344 -----AGAGATGG-----IIGGIIIAII 361

RESULT 4
PVR2 HUMAN
ID PVR2 HUMAN STANDARD; PRT; 538 AA.
AC Q92692; O75455; Q96729;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry
DE mediator B) (HvEB) (Nectin 2) (CD112 antigen).
GN PVR12 OR PRR2 OR HVEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene
RL (PVR), is the true homolog of the murine MPH gene.";
RL Gene 159:267-272(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;
RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT "A cell surface protein with herpesvirus entry activity (HvEB) confers
RT susceptibility to infection by mutants of herpes simplex virus type
RL 1, herpes simplex virus type 2, and pseudorabies virus.";
RL Virology 246:179-189(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Datchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy C., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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Genew; HGNC:9706; PVRL1.
 DR MIM; 600644; -
 DR MIM; 225000; -
 DR MIM; 225060; -
 DR GO; 0016021; C: integral to membrane; NAS.
 DR GO; 0004895; E: cell adhesion receptor activity; NAS.
 DR GO; 0005026; F: coreceptor activity; TAS.
 DR GO; 0006955; F: immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00406; Igv_1.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
 Repeat; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 30
 FT CHAIN 31 517
 FT DOMAIN 31 355
 FT TRANSMEM 356 376
 FT DOMAIN 377 517
 FT DOMAIN 31 141
 FT DOMAIN 149 238
 FT DOMAIN 247 334
 FT DOMAIN 437 444
 FT DOMAIN 445 449
 FT DISULFID 51 124
 FT DISULFID 172 226
 FT DISULFID 269 316
 FT CARBOHYD 36 36
 FT CARBOHYD 72 72
 FT CARBOHYD 139 139
 FT CARBOHYD 202 202
 FT CARBOHYD 286 286
 FT CARBOHYD 297 297
 FT CARBOHYD 307 307
 FT CARBOHYD 332 332
 FT VARSPLIC 335 352
 FT FT 353 517
 FT VARSPLIC 336 458
 FT FT 459 517
 FT VARSPLIC 517 AA; 57158 MW; DF34C8AEC893EB6D CRC64;
 Query Match 11.5%; Score 252.5; DB 1; Length 517;
 Best Local Similarity 25.2%; Pred. No. 7e-11;
 Matches 104; Conservative 59; Mismatches 155; Indels 95; Gaps 19;
 QY 56 IQLNPNQTYFRDPRPLKDSRFLNFSSELKYSLTNVSISDGRYFCOLYDTP-- 113
 DB 78 VAIYNSMGVSLAPYR----ERVELRPSFTDGTIRLSLELEDGVCICEPATPTGN 133
 QY 114 QESYTTITVLPRNLMIDIKD-TAVEGEIEV---NCTAMASKPATIRPFKGNKELK 169
 DB 134 RESQLNLTMNAKPTNWIETGQAVLRKQGDQKVLVATCTTSANGKPPSVVM---ETRLK 190
 QY 170 GKGEVEEW---SDMYTTSOLMKVHKEDDGVFVICOVEHPATGNLQTRY-----LEV 221
 DB 191 GEAYEQEIRNPNGTIVISRYRVLPRGHAHQQLACIV-----NYHMDRFKESLTINV 243
 QY 222 QYKQVHIQ---MTYPLQGLTREDAFELTCEAIGKPPQPMVTWVRVDDMPQHAVLSGP 278
 DB 244 QYEPVETIEGFDGNWYLQRM-----VKLTCKADANPPATEVHTWTLNGLSKPGVEAQRN 298

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FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB0032DDDE3785 CRC64;

Query Match 11.8%; Score 259.5; DB 1; Length 515;
Best Local Similarity 24.5%; Pred. No. 2.2e-11;
Matches 107; Conservative 61; Mismatches 165; Indels 103; Gaps 18;

QY 34 VTVIEGEVATISCCQNKSDSDSVIQLNPNROTIVFRPLKDSRFQLLNFSSELKVS 93
Db 62 ITQVTKATNGSKQN-----VAIYNPAMGVSVLAPYR---ERVEFLRPSFTDGTIRL 111
QY 94 TNVTSISDRGYFCQLYTDP--QSYTYITVLVPRNLMIDIQ-----KDTAVEGER 143
Db 112 SRLEDEGVICBFATPPAGNRSQNLNLYNAKPTNWIETQAVLRKKGKDKV---- 167
QY 144 IEVNCTAMASKPATTIRFKNGKELKSKSEVEW---SDMTVTVSQMLKVHKEDDGVVP 200
Db 168 LVATCTSANGKPPSVSW--ETHLKGAEVQELRNPNGTVTVISRYLVPSPREDHQSL 224
QY 201 ICQVEHPAVTNLQTRY-----LEVQKQPOVHIQ---MTVPLQGLTRGDAFELTCEAI 252
Db 225 ACIV-----NYHMDRFRESLTINVQPEVTIEGFDGNWYLRMD-----VKLTCKAD 272
QY 253 GKQPQVMVTVRVDMPQHAVLSQNLFINN-LNKTDNGTYRCEASNIYKASHDYM 311
Db 273 ANPATEYHTWTLNGLSLPKGVEAQNTLFFRGPINYSNAGTYICEATNPICTRSGQVEVN 332
QY 312 VYDPPTTPIPTTTTTTTTTTTTTTTTTTTTTITLITDSRAGEEG-TIGAVDHVIGGWA---VVV 367
Db 333 ITEPPTPSPP-----EHGRRAGQVPTAIGGVGVSILLVL 368
QY 368 FAMLCLLIILGRYPARKGTFT-----HEAKG-----DDAADATA 405
Db 369 FVGGIVVALCRHRTFKGDYSTKHKVYNGYKAGIPQHPHPMAQNLQYPEDSDDEKKA 428
QY 406 IINAEAGGONNEEKKK 421
Db 429 --GLPGSSYEEREE 442

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RESULT 2

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PVR1 HUMAN STANDARD; PRT; 517 AA.
AC Q1523; Q75465; Q9HBE6; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (Higr)
DE (CD111 antigen).
GN PVR1 OR PRR1 OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabart J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "CDNA characterization and chromosomal localization of a gene related
RT to the poliovirus receptor gene.";

```

```

Gene 155:261-265(1995).
[2] SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE=98279152; PubMed=9616127;
Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
Spear P.G.;
"Entry of alphaherpesviruses mediated by poliovirus receptor-related
protein 1 and poliovirus receptor.";
Science 280:1618-1620(1998).
[3] SEQUENCE FROM N.A. (ISOFORM GAMMA).
MEDLINE=21256041; PubMed=11356977;
Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
Campadelli-Fiume G., Dubreuil P.;
"Novel, soluble isoform of the herpes simplex virus (HSV) receptor
nectin1 (or prr1-Hgr-HvEC) modulates positively and negatively
susceptibility to hsv infection.";
J. Virol. 75:5684-5691(2001).
[4] SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
MEDLINE=2032396; PubMed=10932188;
Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
Helms J.A., Spritz R.A.;
"Mutations of PVR1, encoding a cell-cell adhesion
molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
dysplasia.";
Nat. Genet. 25:427-430(2000).
-!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoform gamma).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=Delta;
IsoId=Q15223-1; Sequence=Displayed;
Name=Alpha;
IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
Name=Gamma;
IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
-!- DISEASE: Defects in PVR1 are a cause of cleft lip/palate-
ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is
responsible for allelic forms known as Margarita island ectodermal
dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930.g.htm".
-----
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EMBL; X76400; CAA53980.2; ALT INIT.
EMBL; AF060231; AAC23798.1; -.
EMBL; AY029539; AAK3124.1; -.
EMBL; AF252867; AAG16648.1; -.
EMBL; AF196768; AAG16648.1; JOINED.
EMBL; AF196769; AAG16648.1; JOINED.
EMBL; AF196770; AAG16648.1; JOINED.
EMBL; AF196771; AAG16648.1; JOINED.
EMBL; AF196774; AAG16649.1; -.
EMBL; AF196768; AAG16649.1; JOINED.
EMBL; AF196769; AAG16649.1; JOINED.
EMBL; AF196770; AAG16649.1; JOINED.
EMBL; AF196771; AAG16649.1; JOINED.
EMBL; AF196772; AAG16649.1; JOINED.
EMBL; AF196773; AAG16649.1; JOINED.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 8.98407 Seconds
(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187b-4

Perfect score: 2197

Sequence: 1 AAPPGRLRLRLRLSAAAL.....TAINAEGGQNGSEKKEKF 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	259.5	11.8	515	1 PVR1_PIG	Q9GL76 sus scrofa
2	252.5	11.5	517	1 PVR1_HUMAN	Q15223 homo sapien
3	243	11.1	530	1 PVR2_MOUSE	P32507 mus musculus
4	238.5	10.9	538	1 PVR2_HUMAN	Q92692 homo sapien
5	237	10.8	417	1 PVR_CERAB	P32506 cercopithec
6	236	10.7	515	1 PVR1_MOUSE	Q9JKE6 mus musculus
7	234	10.7	1088	1 NCA1_XENLA	P16170 xenopus lae
8	232	10.6	344	1 NTRI_MOUSE	Q99PJ0 mus musculus
9	231.5	10.5	417	1 PVR_HUMAN	P15351 homo sapien
10	231	10.5	344	1 NTRI_RAT	Q62718 rattus norv
11	229	10.4	344	1 NTRI_HUMAN	Q9P121 homo sapien
12	225.5	10.3	837	1 NCM2_MOUSE	Q35136 mus musculus
13	222	10.1	837	1 NCM2_HUMAN	O15394 homo sapien
14	222	10.1	1092	1 NCA2_XENLA	P36335 xenopus lae
15	221	10.1	1242	1 NPHN_MOUSE	Q9QZ67 mus musculus
16	220.5	10.0	338	1 LAMP_MOUSE	Q98919 gallus gall
17	220	10.0	337	1 OPMC_CHICK	Q98992 gallus gall
18	218	9.9	583	1 C166_MOUSE	P61490 mus taurus
19	217.5	9.9	345	1 OPMC_BOVIN	P11834 bos taurus
20	215.5	9.8	345	1 OPMC_HUMAN	Q14982 homo sapien
21	214	9.7	588	1 C166_CHICK	P42292 gallus gall
22	211	9.6	847	1 CD22_HUMAN	P20273 homo sapien
23	211	9.6	4391	1 PGBM_HUMAN	P98160 homo sapien
24	209.5	9.5	345	1 OPMC_RAT	P32736 rattus norv
25	209	9.5	353	1 CEPU_CHICK	Q90773 gallus gall
26	207.5	9.4	509	1 SHS1_RAT	P97710 x protein-t
27	207.5	9.4	646	1 MUI8_HUMAN	P43121 homo sapien
28	207	9.4	1493	1 NEOL_MOUSE	P97798 mus musculus
29	206.5	9.4	338	1 NEOL_HUMAN	Q13449 homo sapien
30	206.5	9.4	862	1 CD22_MOUSE	P35329 mus musculus
31	204.5	9.3	338	1 LAMP_RAT	Q62813 rattus norv
32	204	9.3	702	1 CEAS_HUMAN	P06731 homo sapien
33	203.5	9.3	583	1 C166_HUMAN	Q13740 homo sapien

34	203	9.2	1461	1 NEOL_HUMAN	Q2859 homo sapien
35	202	9.2	1443	1 NEOL_CHICK	Q90610 gallus gall
36	198	9.0	1377	1 NEOL_RAT	P97603 rattus norv
37	197	9.0	3707	1 PGBM_MOUSE	Q05793 mus musculus
38	196.5	8.9	1241	1 NPHN_HUMAN	O60500 homo sapien
39	196.5	8.9	1331	1 CTA2_HUMAN	Q9HUC6 homo sapien
40	195	8.9	506	1 SHS1_BOVIN	O46631 bos taurus
41	194	8.8	1091	1 NCA1_CHICK	P13590 gallus gall
42	193	8.8	761	1 NCA2_HUMAN	P13592 homo sapien
43	193	8.8	848	1 NCA1_HUMAN	P13591 homo sapien
44	192.5	8.8	1036	1 AXO1_CHICK	P28685 gallus gall
45	191.5	8.7	853	1 NCA1_BOVIN	P31836 bos taurus

ALIGNMENTS

RESULT 1
PVR1_PIG
ID PVR1_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
DE mediator C) (HveC) (Nectin 1).
GN PVR1L OR PVR1 OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family, is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF308632; AAG30281.1; --
CC HSSP; P06907; 1NEU.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; IG; 2.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG LIKE; 2.
CC Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
CC Repeat; Glycoprotein; Signal.
CC SIGNAL 1 30 POTENTIAL.
CC CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
CC DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 356 376 POTENTIAL.
CC DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 31 141 IG-LIKE V-TYPE.
CC DOMAIN 145 243 IG-LIKE C2-TYPE 1.
CC DOMAIN 247 334 IG-LIKE C2-TYPE 2.
CC DOMAIN 437 443 POLY-GLU.

APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 48.5%; Score 1012.5; DB 2; Length 444;
Best Local Similarity 48.7%; Pred. No. 6.2e-84;
Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
QY 33 PWTSDTVVAGGVVLKQVQKDHEDSLQWNPAAQOTLYFGEKRALDRNRIQLVSTPHE 92
Db 36 PLTQNVTVVEGGTALTCTKVDQNDNTSLQWNPAAQOTLYFDDKKALDRNRIELVRASWEH 95
QY 93 LSIISNVALADEGYTCSTFTMPVTKSLVTLGIPQKPIITGYKSLREKDTATLNC 152
Db 96 LSIISVSDVSLDEGQYTCSTFTMPVTKSLVTLGIPQKPIITGYKSLREKDTATLNC 155
QY 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSVN 212
Db 156 KTSGSKPAADIRWFKNDKIKDVKYLBEDANRKTFTVSSSTLDFRVDSDGVAVICRVD 215
QY 213 HESLKGADRTSQRILEVLYPTAMIRPDPPHREGOKLLHCEGRGNVPQOYLWEKEGS 272
Db 216 HESLNATPQVAMQVLEIHTVPSVKIIPSTPFQEGQPLITCESKGPPLPEPVLTKDGG 275
QY 273 V---PPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSKAYITLVND-----PSPV- 322
Db 276 ELPPDRMVVSGRELNLFLNKTNGTYRCEATNTIGQSAEYVLIVHVDVNTLPTTII 335
QY 323 -----PSSSTY-----HAIIGIVAFIVFLLLIMI 349
Db 336 PSLTTATVTTVAITTSPTTSATTSIRDPNALAGQPDHALIGGIVAVVVFVTLCSIF 395
QY 350 FLGHYLIRHGTLYLTHEAGSDADPADATINAEQGSGGDDKKEYFI 398
Db 396 LLGRLARHKGTYLNEAGGADPADATINAEQSGVNAEKKEYFI 444

RESULT 11

US-08-660-531-5
Sequence 5, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 48.5%; Score 1012.5; DB 3; Length 444;
Best Local Similarity 48.7%; Pred. No. 6.2e-84;
Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
QY 33 PWTSDTVVAGGVVLKQVQKDHEDSLQWNPAAQOTLYFGEKRALDRNRIQLVSTPHE 92
Db 36 PLTQNVTVVEGGTALTCTKVDQNDNTSLQWNPAAQOTLYFDDKKALDRNRIELVRASWEH 95
QY 93 LSIISNVALADEGYTCSTFTMPVTKSLVTLGIPQKPIITGYKSLREKDTATLNC 152
Db 95 LSIISVSDVSLDEGQYTCSTFTMPVTKSLVTLGIPQKPIITGYKSLREKDTATLNC 155
QY 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSVN 212
Db 156 KTSGSKPAADIRWFKNDKIKDVKYLBEDANRKTFTVSSSTLDFRVDSDGVAVICRVD 215
QY 213 HESLKGADRTSQRILEVLYPTAMIRPDPPHREGOKLLHCEGRGNVPQOYLWEKEGS 272
Db 216 HESLNATPQVAMQVLEIHTVPSVKIIPSTPFQEGQPLITCESKGPPLPEPVLTKDGG 275
QY 273 V---PPLKMTQESALIFPFLNKSQSGTYGCTATSNMGSKAYITLVND-----PSPV- 322
Db 276 ELPPDRMVVSGRELNLFLNKTNGTYRCEATNTIGQSAEYVLIVHVDVNTLPTTII 335
QY 323 -----PSSSTY-----HAIIGIVAFIVFLLLIMI 349
Db 336 PSLTTATVTTVAITTSPTTSATTSIRDPNALAGQPDHALIGGIVAVVVFVTLCSIF 395

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1

Query Match 48.5%; Score 1012.5; DB 2; Length 421;
Best Local Similarity 48.7%; Pred. No. 5.7e-84;
Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
QY 33 PWTSDTVVAGTIVLVKCOVKDHEDSSLOWSPNAQOTLYFGEKRALDNRILQVTSPTHE 92
DB 13 PLTONVTVVEGGTAITLCRVQDNDNTSLOWSPNAQOTLYFDDKKALDRNRIELVRASWHE 72
QY 93 LSIISINVALADEGYTCSTFTMPVTRAKSLVTLVGIPOKPIITGYKSSLRKDTATLNC 152
DB 73 LSIISVDSVLSDEGQYTCSTFTMPVTKSKAYLTVLGVPEKPOISGFSPPWMEGLMQLTC 132
QY 153 QSGSKPAARLTWRKGDQELHGEPTFIOEDPNGKTFVSSSVTFQVTRDDGASIVCSVN 212
DB 133 KTSGSKPAADIRFKNDEIKVKYLKEEDANRKTFTVSTLDFRDRSDGAVICRVD 192
QY 213 HESLKGADRTSQRIVLYTPTAMIRPDPPHREGQKLLHCEGRNPVPQOYLWEKGS 272
DB 193 HESLNATPQVAMQVLEIHYTPSVKLIIPSTFPQEGQPLILTCESKGPPLPEPVLTKDGG 252
QY 273 V---PPLKMTQESALIPFFLNKSDSGTYGCTATSNMGSKAYTYLNVND-----PSPV- 322
DB 253 ELPPDRMVVSGRELNLFLNKTNGYRCEATNTIGQSSAEYVLIVHDVPTLLPTTII 312
QY 323 -----PSSSSTY-----HAIGGIVAFIVFLLIMLI 349
DB 313 PSITATVTTTVAITTSPTTSATTSIRDPNALAGQNGPDHALIGGIVAVVFWTLCISIF 372
QY 350 FLGHYLRHKGYTLTHEAKGSDADPADATAIINAEQSGGDDKKEYFI 398
DB 373 LLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEQSQVNAEKKEYFI 421

RESULT 9
US-08-660-531-1
Sequence 1, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-1

Query Match 48.5%; Score 1012.5; DB 3; Length 421;
Best Local Similarity 48.7%; Pred. No. 5.7e-84;
Matches 199; Conservative 70; Mismatches 97; Indels 43; Gaps 4;
QY 33 PWTSDTVVAGTIVLVKCOVKDHEDSSLOWSPNAQOTLYFGEKRALDNRILQVTSPTHE 92
DB 13 PLTONVTVVEGGTAITLCRVQDNDNTSLOWSPNAQOTLYFDDKKALDRNRIELVRASWHE 72
QY 93 LSIISINVALADEGYTCSTFTMPVTRAKSLVTLVGIPOKPIITGYKSSLRKDTATLNC 152
DB 73 LSIISVDSVLSDEGQYTCSTFTMPVTKSKAYLTVLGVPEKPOISGFSPPWMEGLMQLTC 132
QY 153 QSGSKPAARLTWRKGDQELHGEPTFIOEDPNGKTFVSSSVTFQVTRDDGASIVCSVN 212
DB 133 KTSGSKPAADIRFKNDEIKVKYLKEEDANRKTFTVSTLDFRDRSDGAVICRVD 192
QY 213 HESLKGADRTSQRIVLYTPTAMIRPDPPHREGQKLLHCEGRNPVPQOYLWEKGS 272
DB 193 HESLNATPQVAMQVLEIHYTPSVKLIIPSTFPQEGQPLILTCESKGPPLPEPVLTKDGG 252
QY 273 V---PPLKMTQESALIPFFLNKSDSGTYGCTATSNMGSKAYTYLNVND-----PSPV- 322
DB 253 ELPPDRMVVSGRELNLFLNKTNGYRCEATNTIGQSSAEYVLIVHDVPTLLPTTII 312
QY 323 -----PSSSSTY-----HAIGGIVAFIVFLLIMLI 349
DB 313 PSITATVTTTVAITTSPTTSATTSIRDPNALAGQNGPDHALIGGIVAVVFWTLCISIF 372
QY 350 FLGHYLRHKGYTLTHEAKGSDADPADATAIINAEQSGGDDKKEYFI 398
DB 373 LLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEQSQVNAEKKEYFI 421

RESULT 10
US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto

```
Db 301 ATSNWGYTAFTLVNDPSPVSSSTYHAIIGGVAFIVFLDLLILLIFLGHVLIIRHGK 360
QY 361 TYLTAEKSGDDAPDADTAIINAEAGSGGDDKKEYFI 398
Db 361 TYLTAEKSGDDAPDADTAIINAEAGSGGDDKKEYFI 398

RESULT 7
US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917

Query Match 57.0%; Score 1189; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.8e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 ELSISISNVALADEGYTCISFTMPVRTAKSLVTLVIGIPKPIITGYKSLREKDTATLN 151
Db 1 ELSISISNVALADEGYTCISFTMPVRTAKSLVTLVIGIPKPIITGYKSLREKDTATLN 60
QY 152 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGASIVCSV 211
Db 61 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGASIVCSV 120
QY 212 NHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGEGNVPQOYLWEKEG 271
Db 121 NHESLKGADRSQRIEVLVYPTAMIRPDPPHREGOKLLHCEGEGNVPQOYLWEKEG 180
QY 272 SVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVND 318
Db 181 SVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYITLVND 227

RESULT 8
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 6.1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDETVAGTAVLKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDETVAGTAVLKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
QY 361 TYLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 398

RESULT 5
US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match      98.7%; Score 2059; DB 4; Length 432;
Best Local Similarity 92.1%; Pred. No. 2e-179;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQEQDLELGTAPLDEAISVTWSSPDL 60
Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDGYWQEQDLELGTAPLDEAISVTWSSPDL 60
QY 30 ----DSQPWTSDETVAGTAVLKQVKDHEDSSLQWSNPAQOTLYFGEKRALRDNRIQLV 86
Db 61 ASQDSQPWTSDETVAGTAVLKQVKDHEDSSLQWSNPAQOTLYFGEKRALRDNRIQLV 120

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match      100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 6.1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDETVAGTAVLKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDETVAGTAVLKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
QY 361 TYLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDPADADTAIINAEQSGGDDKKEYFI 398

RESULT 6
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; PRIOR FILING DATE: 2001-02-07
; PRIOR FILING DATE: 1999-08-05
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match      95.0%; Score 1982; DB 4; Length 398;
Best Local Similarity 95.0%; Pred. No. 1.9e-172;
Matches 378; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPWTSDETVAGTAVLKQVKDHEDSSL 60
Db 1 MGAPAAASPVLLLLLLACSNAPGANLSQDDSQPWTSDETVAGTAVLKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
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Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRGNPVPQVLYWEKGSVPLKMTQESALIFPLNKSDSGTGCT 300
Db 241 PPHREGOKLLHCEGRGNPVPQVLYWEKGSVPLKMTQESALIFPLNKSDSGTGCT 300
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Db 301 ATSNMGSYKAYTTLNVNDSPVPSSSTYHAIIGGIYVAFIVFLLIMLIFLGHYLRHKG 360
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905/125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-84

Query Match 100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 6,1e-182;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	QWSNPAQOTLYEGRKALRDNRIQLVTSPPHLSISINNALADEGEYTCSTFTMPVATA	120
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DB	121	KSLVTVLGIPQKPIITGYKSSIREKDTATLNCQSSGSPAAALTRWKGDELHGEPTRI	180
QY	181	EDPNGKTTFTVSSSVTFQVTRDDGASIVCSNVHESLKGADSTORSIEVLVPTTAMIRPD	240
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QY	241	PHHPREGOKLLHCEGRGNVPVQQLWKEGSGVPLKMTQESALIFPFLNKSDSCTYCT	300
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QY	301	ATSNMGSKAYTYLNVNDPSPVPSSTVTHAIGGIVAFIVFLIMLIFLGHVLIIRHG	360
DB	301	ATSNMGSKAYTYLNVNDPSPVPSSTVTHAIGGIVAFIVFLIMLIFLGHVLIIRHG	360
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RESULT 4
US-09-902-775A-84
Sequence 84, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902/775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05

; TITLE OF INVENTION: Acids Enrichment

; TITLE OF INVENTION: Acids Encoding the Same

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 14.5581 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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29	228	10.9	338	4	US-09-135-080-8	Sequence 8, Appl
30	225.5	10.8	338	2	US-08-414-657D-42	Sequence 42, Appl
31	225.5	10.8	338	2	US-08-414-657D-43	Sequence 43, Appl
32	225.5	10.8	338	4	US-09-135-080-4	Sequence 4, Appl
33	225	10.8	338	4	US-09-976-594-404	Sequence 404, App
34	224.5	10.8	582	4	US-09-702-705-334	Sequence 334, App
35	224.5	10.8	582	4	US-09-736-457-334	Sequence 334, App
36	224.5	10.8	582	4	US-09-614-124B-334	Sequence 334, App
37	224.5	10.8	582	4	US-09-671-325-334	Sequence 334, App
38	224.5	10.8	582	4	US-09-589-184-334	Sequence 334, App
39	223.5	10.7	583	2	US-08-432-016-2	Sequence 2, Appl
40	223.5	10.7	583	2	US-08-684-594-2	Sequence 2, Appl
41	222	10.6	315	2	US-08-414-657D-47	Sequence 47, Appl
42	221.5	10.6	518	4	US-09-919-172-20	Sequence 20, Appl
43	221.5	10.6	698	2	US-08-602-725-36	Sequence 36, Appl
44	221.5	10.6	734	2	US-08-389-459A-17	Sequence 17, Appl
45	221.5	10.6	734	3	US-08-987-867A-17	Sequence 17, Appl

ALIGNMENTS

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; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

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Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-613-84
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US-09-907-942-84
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; Sequence 84, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-942-84
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Publication No. US20030027143A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/906,838
 CURRENT FILING DATE: 2001-07-16
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
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 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 84
 LENGTH: 398
 TYPE: PRT
 ORGANISM: Homo Sapien

US-09-906-838-84

Query Match 100.0%; Score 2086; DB 10; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7,7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRPAASLHLLLLFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLKQVCKDHEDSSL 60
 Db 1 MGRPAASLHLLLLFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLKQVCKDHEDSSL 60
 QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTSIFTMPVRTA 120
 Db 61 QWSNPAQOTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTSIFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSORIEVLYTPTAMIRPD 240
 Db 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSORIEVLYTPTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNFVPOQYLWEKEGSPPLKMTQESALIPFLNKSQSGTGGCT 300
 Db 241 PPHREGQKLLHCEGRGNFVPOQYLWEKEGSPPLKMTQESALIPFLNKSQSGTGGCT 300
 QY 301 ATSNMGSKAYITLVNNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
 Db 301 ATSNMGSKAYITLVNNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
 QY 361 TYLTAEKSGDDADADATLINAEGSGGDDKKEYFI 398
 Db 361 TYLTAEKSGDDADADATLINAEGSGGDDKKEYFI 398

RESULT 13

US-09-907-613-84
 Sequence 84: Application US/09907613
 Publication No. US20030027145A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/907,613
 CURRENT FILING DATE: 2001-07-17
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048

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Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHSKAGDRSTSORLEVLYTPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHSKAGDRSTSORLEVLYTPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRNPNVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGOKLLHCEGRNPNVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYTILNVNDPSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIHRKG 360
Db 301 ATSNMGSYKAYTILNVNDPSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIHRKG 360
QY 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398

RESULT 11
US-09-906-742-84
; Sequence 84, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

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; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-906-742-84

Query Match
Best Local Similarity 100.0%; Score 2086; DB 10; Length 398;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLFFACCCWAPGGANLSQDDSQPWTSDTETVAGTTLVKQVKDHEDSSL 60
QY 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
Db 61 QWSNPAQOTLYFGKRALRDNRIQLVSTSTPHELSSISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHSKAGDRSTSORLEVLYTPTAMIRPD 240
Db 181 EDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHSKAGDRSTSORLEVLYTPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRNPNVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGOKLLHCEGRNPNVQOYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYTILNVNDPSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIHRKG 360
Db 301 ATSNMGSYKAYTILNVNDPSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIHRKG 360
QY 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDPADADTATLINAEGGSGGDDKKEYFI 398

RESULT 12
US-09-906-838-84
; Sequence 84, Application US/09906838

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; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-841-84

Query Match
Best Local Similarity 100.0%; Score 2086; DB 9; Length 398;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCAPAAASLLLLLLLLLACCAWPGANLSQDSQPWTSDFTVAGGTVVLKCKQKDHEDSSL 60
Db 1 MCAPAAASLLLLLLLLLACCAWPGANLSQDSQPWTSDFTVAGGTVVLKCKQKDHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALDRNIQVLTSTPHELSTISINVALADGEYTCSTFTMPVETA 120
Db 61 QWSNPAQOTLYFGEKRALDRNIQVLTSTPHELSTISINVALADGEYTCSTFTMPVETA 120
QY 121 KSLVTVLGIPQKPIITGYKSSLRKXDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSSLRKXDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKTFVSSSYTFQVTRDDGASIVCSVNHESLKGADRSSTQRIEVLVYPTAMIRPD 240
Db 181 EDPNGKTFVSSSYTFQVTRDDGASIVCSVNHESLKGADRSSTQRIEVLVYPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNVPQVWLKEGKSVPLKMTQESALIFPPLNKSDSGTGCT 300
Db 241 PPHREGQKLLHCEGRGNVPQVWLKEGKSVPLKMTQESALIFPPLNKSDSGTGCT 300
QY 301 ATSNMGSKYATYTLNVNDPSPVSSSTTHAIIIGIVAFIVFLLLIMLIFLGHVLIHKG 360
Db 301 ATSNMGSKYATYTLNVNDPSPVSSSTTHAIIIGIVAFIVFLLLIMLIFLGHVLIHKG 360
QY 361 TYLTHEAKGSDPADPADTAIINAEQSGGDDKEYFI 398
Db 361 TYLTHEAKGSDPADPADTAIINAEQSGGDDKEYFI 398

RESULT 10
US-09-904-011-84
; Sequence 84, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

```

```

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-84

Query Match
100.0%; Score 2086; DB 10; Length 398;

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QY 361 TYLTHEAKGSDADPADTAINAEGGSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDADPADTAINAEGGSGGDDKKEYFI 398

RESULT 8
US-09-907-824-84
; Sequence 84, Application US/09907824
; Publication NO. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
```

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAAPASLLLLLLFACCPAGGANSQDDSQPWSDETAVAGGVVVKCQVKHEDSSL 60
Db 1 MGAAPASLLLLLLFACCPAGGANSQDDSQPWSDETAVAGGVVVKCQVKHEDSSL 60
QY 61 QMSNPAQOTLYFGEKRALDNRILQVSTPHLSISISNVALADEGEYTCSTFTMPVTA 120
Db 61 QMSNPAQOTLYFGEKRALDNRILQVSTPHLSISISNVALADEGEYTCSTFTMPVTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWEKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCQSSGSKPAARLTWEKGDQELHGEPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHSKLGADRSTSORIEVLYTPTAMIRPD 240
Db 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHSKLGADRSTSORIEVLYTPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNPQOVLWEKGSVPPLKMTQESALIPPLFKSDSGTYGCT 300
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QY 301 ATSNMGSKAYTYTLNVNDPSPVPSSTVHAIGGIVAFIVFLLMLFLGHYLRHKG 360
Db 301 ATSNMGSKAYTYTLNVNDPSPVPSSTVHAIGGIVAFIVFLLMLFLGHYLRHKG 360
QY 361 TYLTHEAKGSDADPADTAINAEGGSGGDDKKEYFI 398
Db 361 TYLTHEAKGSDADPADTAINAEGGSGGDDKKEYFI 398

RESULT 9
US-09-907-841-84
; Sequence 84, Application US/09907841
; Publication NO. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
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; PRIOR APPLICATION NUMBER: US 60/095,672
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-778-187B-10

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDTAVAGTTLKQVQKHEDSSL 60
 Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDTAVAGTTLKQVQKHEDSSL 60
 QY 61 QWSNPAQQTLYFGEKRALDNRILQVSTPHELISISINVALADEGETCSIFTMPVRTA 120
 Db 61 QWSNPAQQTLYFGEKRALDNRILQVSTPHELISISINVALADEGETCSIFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
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 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTAMIRPD 240
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 Db 241 PPHREGQKLLHCEGRGNVPQOYLMEKESVPLPKMTQESALIFPPLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHVLIIRHKG 360
 Db 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHVLIIRHKG 360
 QY 361 TYLTHEAKGSDPADADATATINAEQGGSGDDKKEYFI 398
 Db 361 TYLTHEAKGSDPADADATATINAEQGGSGDDKKEYFI 398

RESULT 7

US-09-902-853-84
 ; Sequence 84, Application US/09902853
 ; Publication No. US20020192659A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/902,853
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US/09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 84
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-902-853-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDTAVAGTTLKQVQKHEDSSL 60
 Db 1 MGAPAAASLLLLLLFACCAWPGGANLSQDDSQPMTSDTAVAGTTLKQVQKHEDSSL 60
 QY 61 QWSNPAQQTLYFGEKRALDNRILQVSTPHELISISINVALADEGETCSIFTMPVRTA 120
 Db 61 QWSNPAQQTLYFGEKRALDNRILQVSTPHELISISINVALADEGETCSIFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 Db 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTAMIRPD 240
 Db 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNVPQOYLMEKESVPLPKMTQESALIFPPLNKSDSGTYGCT 300
 Db 241 PPHREGQKLLHCEGRGNVPQOYLMEKESVPLPKMTQESALIFPPLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHVLIIRHKG 360
 Db 301 ATSNMGSKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHVLIIRHKG 360

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,291A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 84
;; LENGTH: 398
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-905-291A-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVVAGGTVVLKQVKKDHEDSSL 60
Db 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVVAGGTVVLKQVKKDHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISINNALADEGEYTCSTFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISINNALADEGEYTCSTFTMPVRTA 120
QY 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSORIEVLYTPTAMIRPD 240
Db 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSORIEVLYTPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNVPVQQYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGRGNVPVQQYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLIMLIFLGHYLRHKG 360
QY 361 TYLTAEKSGDDADPADTAINAEGGSGGDDKKEYFI 398
Db 361 TYLTAEKSGDDADPADTAINAEGGSGGDDKKEYFI 398

RESULT 6

US-09-778-187b-10
; Sequence 10, Application US/09778187B
; Patent No. US20020168712A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow III, William C
; TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
; FILE REFERENCE: 2873-US
; CURRENT APPLICATION NUMBER: US/09/778,187B
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US99/17905
; PRIOR FILING DATE: 1999-08-05

QY 361 TYLTAEKSGDDADPADTAINAEGGSGGDDKKEYFI 398
Db 361 TYLTAEKSGDDADPADTAINAEGGSGGDDKKEYFI 398
RESULT 5
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. US20020164866A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVVAGGTVVLKQVKKDHEDSSL 60
Db 1 MGAPAAASLLLLLLFACCCWAPGAGANLSODDSQPWTSDETVVAGGTVVLKQVKKDHEDSSL 60
QY 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISINNALADEGEYTCSTFTMPVRTA 120
Db 61 QWSNPAQOTLYFGEKRALDRNRIQLVTSIPHELSSISINNALADEGEYTCSTFTMPVRTA 120
QY 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPOKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSORIEVLYTPTAMIRPD 240
Db 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSORIEVLYTPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNVPVQQYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGRGNVPVQQYLWEKGSVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLIMLIFLGHYLRHKG 360
Db 301 ATSNMGSKAYTYTLNVNDSPVPSSTTHAIIIGGIVAFIVFLIMLIFLGHYLRHKG 360
QY 361 TYLTAEKSGDDADPADTAINAEGGSGGDDKKEYFI 398
Db 361 TYLTAEKSGDDADPADTAINAEGGSGGDDKKEYFI 398

QY 361 TYLTHEAKSGDDADPADTATINAEQSGGDDKKEYFI 398
 Db 361 TYLTHEAKSGDDADPADTATINAEQSGGDDKKEYFI 398

RESULT 3

US-09-909-088B-84
 ; Sequence 84, Application US/09909088B
 ; Patent No. US20020146709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/909, 088B
 ; CURRENT FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 84

LENGTH: 398
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-909-088B-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
 Best Local Similarity 100.0%; Pred. No. 7.7e-162;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPASLLLLLLFACCCWAPGGANLSQDDSQWTSDETVVAGTVVVKQVKDHEDSSL 60
 Db 1 MGAPASLLLLLLFACCCWAPGGANLSQDDSQWTSDETVVAGTVVVKQVKDHEDSSL 60
 QY 61 QMSNPAQQTLYFGEKEALNRRIQLVTSFHELSISISNVALADEGEYTCISFTMPVRTA 120
 Db 61 QMSNPAQQTLYFGEKEALNRRIQLVTSFHELSISISNVALADEGEYTCISFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCSSGSKPAARLTWRKQDELHGEPTRIQ 180
 Db 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCSSGSKPAARLTWRKQDELHGEPTRIQ 180
 QY 181 EDNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSORIEVLYTPTAMIRPD 240
 Db 181 EDNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSORIEVLYTPTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNPVPQOYLWEKEGSPVPLKMTQESALIFPELNKSDSGTYGCT 300
 Db 241 PPHREGQKLLHCEGRGNPVPQOYLWEKEGSPVPLKMTQESALIFPELNKSDSGTYGCT 300
 QY 301 ATSNMGSYKAYTYLNVNDSPVSSSTYHAIIGGIVAFIVFILLMLIFLGHYLRHKG 360
 Db 301 ATSNMGSYKAYTYLNVNDSPVSSSTYHAIIGGIVAFIVFILLMLIFLGHYLRHKG 360
 QY 361 TYLTHEAKSGDDADPADTATINAEQSGGDDKKEYFI 398
 Db 361 TYLTHEAKSGDDADPADTATINAEQSGGDDKKEYFI 398

RESULT 4

US-09-905-291A-84
 ; Sequence 84, Application US/09905291A
 ; Patent No. US20020160374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-745-763-102

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSPWTSDETVVAGTGVVLCQVKDHDSSSL 60
DB 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSPWTSDETVVAGTGVVLCQVKDHDSSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHLSISISNVALADEGEYTCISFTMPVRTA 120
DB 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHLSISISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
DB 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHSKLGADRSQSRIEVLVYPTAMIRPD 240
DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHSKLGADRSQSRIEVLVYPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRNPVPQOYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGOKLLHCEGRNPVPQOYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
DB 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
QY 361 TYLTHEAKSGDDAPDADTAIINAEQSGGDDKKYFI 398
DB 361 TYLTHEAKSGDDAPDADTAIINAEQSGGDDKKYFI 398

RESULT 2

US-09-909-320-84
Sequence 84, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-320-84

Query Match 100.0%; Score 2086; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.7e-162;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSPWTSDETVVAGTGVVLCQVKDHDSSSL 60
DB 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSPWTSDETVVAGTGVVLCQVKDHDSSSL 60
QY 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHLSISISNVALADEGEYTCISFTMPVRTA 120
DB 61 QWSNPAQOTLYFGEKRALRDNRIQLVSTPHLSISISNVALADEGEYTCISFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
DB 121 KSLVTVLGIPQKPIITGYKSLREKDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHSKLGADRSQSRIEVLVYPTAMIRPD 240
DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHSKLGADRSQSRIEVLVYPTAMIRPD 240
QY 241 PPHREGOKLLHCEGRNPVPQOYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCT 300
DB 241 PPHREGOKLLHCEGRNPVPQOYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
DB 301 ATSNMGSKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:35:05 ; Search time 33.8124 Seconds
(without alignments)
3286.999 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPASLLLLLLLFFACWA.....ATINAGGSGGDKKEYFI 398

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	398	9	US-09-745-763-102
2	2086	100.0	398	9	US-09-909-320-84
3	2086	100.0	398	9	US-09-909-088B-84
4	2086	100.0	398	9	US-09-905-291A-84
5	2086	100.0	398	9	US-09-778-510-6
6	2086	100.0	398	9	US-09-778-187B-10
7	2086	100.0	398	9	US-09-902-853-84
8	2086	100.0	398	9	US-09-907-824-84
9	2086	100.0	398	9	US-09-907-841-84
10	2086	100.0	398	10	US-09-904-011-84
11	2086	100.0	398	10	US-09-906-742-84
12	2086	100.0	398	10	US-09-906-838-84
13	2086	100.0	398	10	US-09-907-613-84
14	2086	100.0	398	10	US-09-907-942-84
15	2086	100.0	398	10	US-09-904-859-84

16	2086	100.0	398	10	US-09-909-204-84	Sequence 84, Appl
17	2086	100.0	398	10	US-09-904-820-84	Sequence 84, Appl
18	2086	100.0	398	10	US-09-904-786-84	Sequence 84, Appl
19	2086	100.0	398	10	US-09-906-646-84	Sequence 84, Appl
20	2086	100.0	398	10	US-09-906-700-84	Sequence 84, Appl
21	2086	100.0	398	10	US-09-903-786-84	Sequence 84, Appl
22	2086	100.0	398	10	US-09-902-903-84	Sequence 84, Appl
23	2086	100.0	398	10	US-09-903-749A-84	Sequence 84, Appl
24	2086	100.0	398	10	US-09-904-119-84	Sequence 84, Appl
25	2086	100.0	398	10	US-09-904-956-84	Sequence 84, Appl
26	2086	100.0	398	10	US-09-902-736-84	Sequence 84, Appl
27	2086	100.0	398	10	US-09-907-794-84	Sequence 84, Appl
28	2086	100.0	398	10	US-09-903-943-84	Sequence 84, Appl
29	2086	100.0	398	10	US-09-904-462-84	Sequence 84, Appl
30	2086	100.0	398	10	US-09-907-925-84	Sequence 84, Appl
31	2086	100.0	398	10	US-09-902-692-84	Sequence 84, Appl
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33	2086	100.0	398	10	US-09-905-056-84	Sequence 84, Appl
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35	2086	100.0	398	10	US-09-904-583-84	Sequence 84, Appl
36	2086	100.0	398	10	US-09-905-381-84	Sequence 84, Appl
37	2086	100.0	398	10	US-09-905-088-84	Sequence 84, Appl
38	2086	100.0	398	10	US-09-907-575-84	Sequence 84, Appl
39	2086	100.0	398	10	US-09-905-075-84	Sequence 84, Appl
40	2086	100.0	398	10	US-09-902-759-84	Sequence 84, Appl
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43	2086	100.0	398	10	US-09-907-979-84	Sequence 84, Appl
44	2086	100.0	398	10	US-09-902-615-84	Sequence 84, Appl
45	2086	100.0	398	10	US-09-903-925-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1

US-09-745-763-102

; Sequence 102, Application US/09745763

; Patent No. US20020065394A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John M.

; Lavallie, Edward R.

; Collins-Racie, Lisa A.

; Evans, Cheryl

; Merberg, David

; Treacy, Maurice

; Spaulding, Vikki

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 219

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/745.763

; FILING DATE: 18-Jun-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Sprunger, Suzanne A.

; REGISTRATION NUMBER: 41,323

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8284

; TELEFAX: (617) 876-5851

Thu May 27 10:42:49 2004

Query Match 100.0%; Score 2086; DB 6; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.5e-149;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	241	PPHREGOKLLHCEGRGNVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCT	300
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Search completed: May 27, 2004, 09:31:27
Job time : 46.5528 secs

PN US2003032156-A1.
XX 13-FEB-2003.
XX 06-MAY-2002; 2002US-00140474.
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US016824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 29-OCT-1998; 98WO-US022992.
XX 20-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 13-SEP-1999; 99WO-US020594.
XX 08-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
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XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030939.
XX 22-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005746.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006319.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 28-JUL-2000; 2000WO-US020710.
XX 11-AUG-2000; 2000WO-US022031.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017032.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019632.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski FJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-341980/32.

DR N-PSDB; ACD24026.

XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.

XX Claim 12; Fig 348; 650pp; English.

CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

XX Sequence 398 AA;

PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US018824.
 PR 17-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-DEC-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028564.
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 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 DR WPI: 2003-328338/31.
 DR N-PSDB; ACAS8964.

XX Isolated nucleic acid useful for e.g., treating pathological disorders
 PT encodes a secreted or transmembrane protein.
 PS Claim 12; Fig 32; 473pp; English.

XX The invention relates to human PRO polypeptides (secreted or

CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC PRO polypeptides and polynucleotides can be used in treating pathological
 CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
 CC disorders and in therapeutic treatment of disorders involving protein
 CC secretion by the pancreas, including diabetes. They can also be used in
 CC treating disorders associated with the preservation and maintenance of
 CC gastrointestinal mucosa and the repair of acute and chronic mucosal
 CC lesions, and skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g., psoriasis, epithelial cancers such as lung
 CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
 CC The sequences can be used as molecular markers for protein
 CC electrophoresis purposes and can be utilised in protein-binding
 CC assays, biochemical screening assays, immunoassays and cell-based assays.
 CC This sequence represents a human PRO polypeptide of the invention
 XX

SQ Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 6; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY - MGAPAAALLLLLLFACCAWAPGGANLSQDDSQPWTSDTAVAGTVVLKQVKHEDSSL 60
 DB - MGAPAAALLLLLLFACCAWAPGGANLSQDDSQPWTSDTAVAGTVVLKQVKHEDSSL 60
 QY 61 QWSNPAQQTLYFGKRALRDNRIOIQTSTPHELSTISINVALADEGYTCSTFTMPVETA 120
 DB 61 QWSNPAQQTLYFGKRALRDNRIOIQTSTPHELSTISINVALADEGYTCSTFTMPVETA 120
 QY 121 KSLVTVLGIPQKIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPETRIQ 180
 DB 121 KSLVTVLGIPQKIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPETRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSORSORIEVLYTPTAMIRPD 240
 DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSORSORIEVLYTPTAMIRPD 240
 QY 241 PPHREGOKLLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSTYGTCT 300
 DB 241 PPHREGOKLLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSTYGTCT 300
 QY 301 ATSNMGSYKAYTYLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
 DB 301 ATSNMGSYKAYTYLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
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 DB 361 TYLTAEAKGSDADPADTAIINAEKGSGGDDKKEYFI 398

RESULT 15

ABO17789

ID ABO17789 standard; protein; 398 AA.

XX ABO17789;

XX ABO17789;

XX 26-AUG-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO258.

DE Human; secreted and transmembrane protein; PRO; antiinflammatory;
 XX antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing.

OS Homo sapiens.

XX

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytostatic; antiangiogenic; hypotensive; vulnery;
 KW antiarteriosclerotic.

XX
 OS Homo sapiens.

XX
 PN W0200208284-A2.

XX
 PD 31-JAN-2002.

XX
 PF 09-JUL-2001; 2001WO-US021735.

XX
 PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222595P.

PR 17-AUG-2000; 2000US-0224365P.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242322P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 01-JUN-2001; 2001WO-US017443.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX
 PS Claim 11; Fig 44; 567pp; English.

XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention

XX
 SQ Sequence 398 AA;

Query Match 100.0%; Score 2086; DB 5; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAASLLLLLLFACCCWAPCGANLSQDDSPWTSDETVVAGGVVLCQVKDHEDSSL 60

Db 1 MGAPAAASLLLLLLFACCCWAPCGANLSQDDSPWTSDETVVAGGVVLCQVKDHEDSSL 60

QY 61 QWSNPAQQTLYFGEKRALRDNRILQVSTPHLSISINVALADEGYTCSTFTMPVRTA 120

Db 61 QWSNPAQQTLYFGEKRALRDNRILQVSTPHLSISINVALADEGYTCSTFTMPVRTA 120

QY 121 KSLVTVLGIPQPIITGYKSSLRKXDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ 180

Db 121 KSLVTVLGIPQPIITGYKSSLRKXDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ 180

QY 181 EDPNGKTFVSSVTFQVTRDDGASIVCSNVHESLKADRTSQRIRVLYPTAMIRPD 240

Db 181 EDPNGKTFVSSVTFQVTRDDGASIVCSNVHESLKADRTSQRIRVLYPTAMIRPD 240

QY 241 PPHREGQKLLHCEGRGNVPVQQYLWEKESVPLKMTQESALIFPFLNKSDSTGYGCT 300

Db 241 PPHREGQKLLHCEGRGNVPVQQYLWEKESVPLKMTQESALIFPFLNKSDSTGYGCT 300

QY 301 ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360

Db 301 ATSNMGSKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360

QY 361 TYLTHEAKGSDPADADTAITNAEGGQSGDDKKEYFI 398

Db 361 TYLTHEAKGSDPADADTAITNAEGGQSGDDKKEYFI 398

RESULT 13

ABP61823

ID ABP61823 standard; protein; 398 AA.

XX AC ABP61823;

XX DT 04-OCT-2002 (first entry)

XX DE Human polypeptide SEQ ID NO 177.

XX Human; cytostatic; antirheumatic; antiarthritic; vulnery; analgesic;
 KW antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
 KW neuroprotective; nootropic; osteopathic; haemostatic; vasotropic;
 KW antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;
 KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;
 KW cytokine; cell proliferation; cell differentiation; autoimmune disease;
 KW stem cell; growth factor; nervous system disease; neuropathy;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW osteoporosis; severe combined immunodeficiency; SCID; infection;
 KW multiple sclerosis; rheumatoid arthritis; gene therapy.

XX OS Homo sapiens.

XX

```
Db 301 ATSNMGSKAYITLVNDSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHG 360
QY 361 TYLTAEAGSDDAPDADTAIINAEQSGGDDKKEYFI 398
Db 361 TYLTAEAGSDDAPDADTAIINAEQSGGDDKKEYFI 398

RESULT 11
ID ABB84838 standard; protein; 398 AA.
XX ABB84838;
XX
XX 16-MAY-2002 (first entry)
XX Human PRO258 protein sequence SEQ ID NO:44.
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
XX vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
XX Homo sapiens.
XX WO200200690-A2.
XX
XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US019692.
XX
XX 23-JUN-2000; 2000US-0213637P.
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 28-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 22-JAN-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 01-MAR-2001; 2001WO-US006520.
XX 09-MAR-2001; 2001WO-US006666.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 25-MAY-2001; 2001US-00866034.
XX 30-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 01-JUN-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX (GETH ) GENENTECH INC.
XX
```

```
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88093.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 44; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The PRO polynucleotides have applications in molecular biology,
XX including use as hybridisation probes, and in chromosome and gene
XX mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX exemplification of the present invention
XX
XX Sequence 398 AA;
```

```
Query Match 100.0%; Score 2086; DB 5; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.5e-149;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSQPWTSDTAVAGTVVLKQVKDHEDSSL 60
Db 1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSQPWTSDTAVAGTVVLKQVKDHEDSSL 60
QY 61 QWSNPAQQTLYFGEKRALRDNRILQVTSFPHLSISISNVALADEGYTCSTFTMPVRTA 120
Db 61 QWSNPAQQTLYFGEKRALRDNRILQVTSFPHLSISISNVALADEGYTCSTFTMPVRTA 120
QY 121 KSLVTVLGIPQKIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ 180
Db 121 KSLVTVLGIPQKIITGYKSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGPTRIQ 180
QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTSORIEVLVPTAMIRPD 240
Db 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSVNHESLKADRSSTSORIEVLVPTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNPVPQVLMKEGKSVPLKMTQESALIFPFLNKSDSGTYGCT 300
Db 241 PPHREGQKLLHCEGRGNPVPQVLMKEGKSVPLKMTQESALIFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYITLVNDSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHG 360
Db 301 ATSNMGSKAYITLVNDSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHG 360
QY 361 TYLTAEAGSDDAPDADTAIINAEQSGGDDKKEYFI 398
Db 361 TYLTAEAGSDDAPDADTAIINAEQSGGDDKKEYFI 398

RESULT 12
ID ABB95444 standard; protein; 398 AA.
XX ABB95444;
XX
XX 19-JUL-2002 (first entry)
XX Human angiogenesis related protein PRO258 SEQ ID NO: 44.
XX
```

QY 1 MGAPAAALLLLLLLFPACWAPGANLSQDDSQPMTSDTAVAGGTWLVKCVKHEDSSL 60
 DB 1 MGAPAAALLLLLLLFPACWAPGANLSQDDSQPMTSDTAVAGGTWLVKCVKHEDSSL 60
 QY 61 QWSNPAQOTLYFGEKRALDRNRIOQVTSSTPHELSSISNVALADEGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDRNRIOQVTSSTPHELSSISNVALADEGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSLKGDADSTSORIEVLYTPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSLKGDADSTSORIEVLYTPTAMIRPD 240
 QY 241 PPHREGOKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGOKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDSPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
 DB 301 ATSNMGSKAYTYTLNVNDSPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360
 QY 361 TYLTPEAKSGDDAPDADTAIINAEGQSGGDDKKEYFI 398
 DB 361 TYLTPEAKSGDDAPDADTAIINAEGQSGGDDKKEYFI 398
 RESULT 10
 ID AAB53083
 XX AAB53083 standard; protein; 398 AA.
 AC AAB53083;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO258, SEQ ID NO:101.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US000219.
 XX
 XX 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 05-OCT-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028409.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.

(GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 Godowski FJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 WPI: 2001-090793/10.
 DR N-PSDB; AAC97445.
 XX
 New isolated nucleic acid for producing a PRO polypeptide, analyzing
 genetic disorders and treating cardiovascular, endothelial or angiogenic
 disorders, such as atherosclerosis, wounds or cancer.
 PS Claim 69; Fig 40; 23pp; English.
 XX
 The invention relates to novel human angiogenesis-associated proteins
 designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 PRO proteins. The invention also relates to vectors and host cells
 comprising a PRO nucleic acid, the recombinant production of a PRO
 protein, PRO antibodies specific for a PRO protein, fusion proteins
 comprising a PRO protein, agonists or antagonists of a PRO protein, and
 compounds which inhibit the expression of a PRO gene. The invention
 additionally encompasses methods of identifying modulators of PRO
 expression or activity; diagnosing a cardiovascular, endothelial or
 angiogenic disorder, or a susceptibility to such a disorder by detecting
 mutations in a PRO gene, or the expression level of a PRO gene within a
 particular tissue; treating a cardiovascular, endothelial or angiogenic
 disorder via the administration of a PRO protein, PRO nucleic acid, or
 PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 administration of a PRO protein, or an agonist or antagonist thereof. PRO
 nucleic acids, PRO proteins, or antibodies against PRO proteins, PRO
 agonists and PRO antagonists may be used as therapeutic agents to treat
 cardiovascular, endothelial or angiogenic disorders, such as
 atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 disease, or stroke. PRO nucleic acids are additionally useful in the
 recombinant production of PRO proteins, as hybridisation probes to screen
 libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 genes encoding PRO proteins, to analyse genetic disorders, and in gene
 therapy. PRO nucleic acids can also be used to produce transgenic animals
 useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PRO protein of the invention
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 4; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAALLLLLLLFPACWAPGANLSQDDSQPMTSDTAVAGGTWLVKCVKHEDSSL 60
 DB 1 MGAPAAALLLLLLLFPACWAPGANLSQDDSQPMTSDTAVAGGTWLVKCVKHEDSSL 60
 QY 61 QWSNPAQOTLYFGEKRALDRNRIOQVTSSTPHELSSISNVALADEGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDRNRIOQVTSSTPHELSSISNVALADEGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSLKGDADSTSORIEVLYTPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHSLKGDADSTSORIEVLYTPTAMIRPD 240
 QY 241 PPHREGOKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGOKLLHCEGRGNVPVQOYLWEKSGVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYTYTLNVNDSPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKG 360

CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping
XX Sequence 398 AA;
SQ Query Match 100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.5e-149; Indels 0; Gaps 0;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAPAAASLLLLLLFACCAWAGANLSDQDSQFVTSVAGGTVVLCQVKHEDSSL 60
Db 1 MGAPAAASLLLLLLFACCAWAGANLSDQDSQFVTSVAGGTVVLCQVKHEDSSL 60
QY 61 QNSNPAQOTLYGEXKRALDNRIOQVTSVPHLSISISNVALADGEYTCSTFTMPVRTA 120
Db 61 QNSNPAQOTLYGEXKRALDNRIOQVTSVPHLSISISNVALADGEYTCSTFTMPVRTA 120
QY 121 KSLVTVLGIPOKPIITGYKSLUREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
Db 121 KSLVTVLGIPOKPIITGYKSLUREKDTATLNCQSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYFTTAMIRPD 240
Db 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYFTTAMIRPD 240
QY 241 PPHREGOKLLHCGRGNPVPQOVLWEKGSVPPLKMTQESALFPFLNKSDSGTYGCT 300
Db 241 PPHREGOKLLHCGRGNPVPQOVLWEKGSVPPLKMTQESALFPFLNKSDSGTYGCT 300
QY 301 ATSNMGSKAYITLVNDPSPVSSSTVHAIGGIVAFIVFLLMLIFLGHYLRHKG 360
Db 301 ATSNMGSKAYITLVNDPSPVSSSTVHAIGGIVAFIVFLLMLIFLGHYLRHKG 360
QY 361 TYLTAEKSGDDAPADTAIINAEQSGSGDDKKYFI 398
Db 361 TYLTAEKSGDDAPADTAIINAEQSGSGDDKKYFI 398
RESULT 9
AAU12345
ID AAU12345 standard; protein; 398 AA.
XX
AC AAU12345;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO258 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 02-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.

30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff B, Gao W;
PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21417.
XX
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 348; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 398 AA;
Query Match 100.0%; Score 2086; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.5e-149;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human.
 XX Homo sapiens.
 OS
 PN WO200015796-A2.
 XX
 PD 23-MAR-2000.
 XX
 XX
 PF 15-SEP-1999; 99WO-US021090.
 XX
 PR 16-SEP-1998; 98WO-US019330.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 XX
 DR WPI: 2000-271434/23.
 XX
 DR N-PSDB; ADC78403.
 XX
 PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX
 PS Claim 12; SEQ ID NO 84; 355pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, rheumatoid arthritis, multiple
 CC cartilage formation, angiogenesis, asthma, thrombosis, bone and/or
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO protein of the invention.
 XX
 SQ Sequence 398 AA;

Query Match
 Best Local Similarity 100.0%; Score 2086; DB 3; Length 398;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAAALLLLLLLACWAPGAGNLQDDSPWTSDETAVAGTFLKQVKHEDSSL 60
 DB 1 MGAPAAALLLLLLLACWAPGAGNLQDDSPWTSDETAVAGTFLKQVKHEDSSL 60
 QY 61 QWSNPAQQLTFEGEKRALDNRIQVTSPTHELSSISNVALADRGVTCSTFTMPVETA 120
 DB 61 QWSNPAQQLTFEGEKRALDNRIQVTSPTHELSSISNVALADRGVTCSTFTMPVETA 120
 QY 121 KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGKPAARLTWRKGDQELHGPTRIQ 180
 DB 121 KSLVTVLGIPQPIITGYKSSLRKDTATLNCQSSGKPAARLTWRKGDQELHGPTRIQ 180
 QY 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSNVHESLKGADRSQRIEVLVYFTAMIRPD 240
 DB 181 EDPNGKTFVSSSVTFQVTRDDGASIVCSNVHESLKGADRSQRIEVLVYFTAMIRPD 240
 QY 241 PPHREGKLLHCEGRGNVPQVYLWEKESGVPPLKMTQSNALIFPLNKSDSTGYCT 300
 DB 241 PPHREGKLLHCEGRGNVPQVYLWEKESGVPPLKMTQSNALIFPLNKSDSTGYCT 300
 QY 301 ATSNMGSKAYTYTLNVNDFSPVPSSSSYTHALIGIVAFIVFLLIMLIFLGHYLRHKG 360
 DB 301 ATSNMGSKAYTYTLNVNDFSPVPSSSSYTHALIGIVAFIVFLLIMLIFLGHYLRHKG 360

QY 361 TYLTHEAKGSDADPADTALINAEGGSGGDDKKEYFI 398
 DB 361 TYLTHEAKGSDADPADTALINAEGGSGGDDKKEYFI 398

RESULT 8
 AAB80226
 ID AAB80226 standard; protein; 398 AA.
 XX
 AC AAB80226;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO258 protein.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiac;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000WO-US004414.
 XX
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather CP, Pan J, Paoni NF, Roy NA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 DR WPI: 2001-081051/09.
 DR N-PSDB; AAF72387.
 PT
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).
 XX
 PS Claim 1; Fig 32; 393pp; English.
 CC
 CC The present sequence is one of sixty one novel secreted and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful for treating skin
 CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory

KW Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
 KW neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;
 KW dementia; epilepsy; schizophrenia; peripheral nerve injury;
 KW diabetic neuropathy.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide
 FT 25..398
 FT /label= ACAM
 XX
 PN WO200032633-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US028878.
 XX
 PR 02-DEC-1998; 98US-00203462.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Hoekstra DM, Loughney K, Stauton DE, Vazeux R;
 DR WPI; 2000-422952/36.
 DR N-PSDB; AAY94403.
 XX
 PT Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful
 PT for diagnosing, preventing and treating diseases associated with ACAM
 PT expression and activity, e.g. epilepsy and schizophrenia.
 XX
 PS Claim 5; Page 149-150; 187pp; English.
 CC
 CC The present sequence is a novel adhesion molecule, designated ACAM. The
 CC full-length nucleotide sequence was identified in clone ACAM#4 of a human
 CC foetal brain library. The polypeptide is 100% homologous to the
 CC polypeptide encoded by clone ACAM#6 (AAA30423) from the same library
 CC except that it contains a 34 amino acid deletion. It is believed to
 CC correspond to an alternative form of ACAM. The nucleotide sequence and
 CC the protein it encodes may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate ACAM expression and
 CC activity such as dementia, epilepsy, schizophrenia, peripheral nerve
 CC injuries and diabetic neuropathies. They may be used to rectify mutations
 CC or deletions in a patient's genome that affect the activity of ACAM or to
 CC supplement insufficient ACAM production in a patient. The nucleotide
 CC sequence may be integrated into an expression vector and inserted into a
 CC host cell for protein expression in vitro or in vivo. Conversely,
 CC antisense nucleic acid molecules may be administered to down-regulate
 CC ACAM expression. The nucleotide sequence may also be used as a DNA probe
 CC in diagnostic assays (e.g. PCR) to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples, and hence determine which
 CC patients may be in need of restorative therapy. ACAM polypeptides may be
 CC used as antigens in the production of antibodies against ACAM and in
 CC assays to identify modulators (agonists and antagonists) of ACAM
 CC expression and activity
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 3; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAALLLLLLLACCAWPGANLSDQSPWTSDETVAGGTVLKCQVKHEDSSL 60
 DB 1 MGAPAAALLLLLLLACCAWPGANLSDQSPWTSDETVAGGTVLKCQVKHEDSSL 60
 QY 61 QWSNPAQQLTYFGEKRALDRNRIQLVTSPPHELSISINVALADGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQQLTYFGEKRALDRNRIQLVTSPPHELSISINVALADGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPOKPIITGYKSSLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180

DB 121 KSLVTVLGIPOKPIITGYKSSLREKDTATLNCSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADSTSORIEVLYTPTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADSTSORIEVLYTPTAMIRPD 240
 QY 241 PPHPREGQKLLHCEGRGNPVPQOYLMEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHPREGQKLLHCEGRGNPVPQOYLMEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSKAYITLNVNDPSPVSSSTYTHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
 DB 301 ATSNMGSKAYITLNVNDPSPVSSSTYTHAIIGGIVAFIVFLLLIMLIFLGHYLRHKG 360
 QY 361 TYLTHEAKGSDDADPDADTAIINAEKGSGGGDDKKEYFI 398
 DB 361 TYLTHEAKGSDDADPDADTAIINAEKGSGGGDDKKEYFI 398
 RESULT 5
 AAY69288
 ID AAY69288 standard; protein; 398 AA.
 XX
 AC AAY69288;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of extracellular form of human B7-1 (CD80).
 XX
 KW Short form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
 KW CD28; CTLA4; T cell surface receptor; cytokine production;
 KW cell proliferation; T cell; infection; autoimmune disease; inflammation;
 KW quality assurance; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200008057-A2.
 XX
 PD 17-FEB-2000.
 XX
 PF 05-AUG-1999; 99WO-US017906.
 XX
 PR 07-AUG-1998; 98US-0095663P.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Baum PR;
 XX
 DR WPI; 2000-205674/18.
 DR N-PSDB; AAZ61418.
 XX
 PT Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
 PT costimulatory molecules for therapeutics against infections, autoimmune
 PT diseases and inflammation.
 XX
 PS Claim 8; Page 47-48; 57pp; English.
 XX
 CC The present sequence represents the short extracellular form of human B7-
 CC 1 (CD80). B7-1 is a T-cell costimulatory molecule that is found on the
 CC surface of antigen presenting cells (APCs). CD28 and CTLA4 are its T cell
 CC surface receptors. B7-1 interacts with CD28 to signal cytokine
 CC production, cell proliferation, and the generation of effector and memory
 CC T cells. Disorders mediated by interaction of B7-1 and its binding
 CC partner, such as infections, autoimmune diseases and inflammation, are
 CC treated by administering B7L-1 to the disordered mammal. B7L-1
 CC polypeptides are useful to separate cells expressing a protein to which
 CC it binds and to measure the biological activity of LDCAM polypeptides.
 CC They can also be used as reagents for conducting quality assurance
 CC studies e.g., to monitor shelf life and stability of proteins to which it
 CC binds, and as carriers for delivering agents attached to cells bearing
 CC its counter structure, LDCAM or other cell receptors. They are also
 CC useful as a research tool for studying T-cell signalling and
 CC proliferation. They are employed in in vitro assays for detecting

XX		Secreted protein; transmembrane protein; human; enterocolitis;
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;	
KW	congenital microvillus atrophy; skin disease; cell growth;	
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;	
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;	
KW	dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;	
KW	wound healing; tissue repair.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9914328-A2.	
XX		
PD	25-MAR-1999.	
XX		
PF	16-SEP-1998; 98WO-US019330.	
PR	17-SEP-1997; 97US-0059113P.	
PR	17-SEP-1997; 97US-0059115P.	
PR	17-SEP-1997; 97US-0059117P.	
PR	17-SEP-1997; 97US-0059119P.	
PR	17-SEP-1997; 97US-0059121P.	
PR	17-SEP-1997; 97US-0059122P.	
PR	17-SEP-1997; 97US-0059184P.	
PR	18-SEP-1997; 97US-0059263P.	
PR	18-SEP-1997; 97US-0059266P.	
PR	15-OCT-1997; 97US-0062125P.	
PR	17-OCT-1997; 97US-0062285P.	
PR	17-OCT-1997; 97US-0062287P.	
PR	21-OCT-1997; 97US-0063486P.	
PR	24-OCT-1997; 97US-0062814P.	
PR	24-OCT-1997; 97US-0062816P.	
PR	24-OCT-1997; 97US-0063045P.	
PR	24-OCT-1997; 97US-0063120P.	
PR	24-OCT-1997; 97US-0063121P.	
PR	24-OCT-1997; 97US-0063127P.	
PR	24-OCT-1997; 97US-0063128P.	
PR	27-OCT-1997; 97US-0063327P.	
PR	27-OCT-1997; 97US-0063329P.	
PR	28-OCT-1997; 97US-0063541P.	
PR	28-OCT-1997; 97US-0063542P.	
PR	28-OCT-1997; 97US-0063544P.	
PR	28-OCT-1997; 97US-0063549P.	
PR	28-OCT-1997; 97US-0063550P.	
PR	28-OCT-1997; 97US-0063564P.	
PR	29-OCT-1997; 97US-0063435P.	
PR	29-OCT-1997; 97US-0063704P.	
PR	29-OCT-1997; 97US-0063732P.	
PR	29-OCT-1997; 97US-0063734P.	
PR	29-OCT-1997; 97US-0063735P.	
PR	29-OCT-1997; 97US-0063738P.	
PR	31-OCT-1997; 97US-0064215P.	
PR	31-OCT-1997; 97US-0063870P.	
PR	31-OCT-1997; 97US-0064103P.	
PR	03-NOV-1997; 97US-0064248P.	
PR	07-NOV-1997; 97US-0064809P.	
PR	12-NOV-1997; 97US-0065186P.	
PR	17-NOV-1997; 97US-0065846P.	
PR	18-NOV-1997; 97US-0065693P.	
PR	21-NOV-1997; 97US-0066120P.	
PR	21-NOV-1997; 97US-0066364P.	
PR	24-NOV-1997; 97US-0066453P.	
PR	24-NOV-1997; 97US-0066466P.	
PR	24-NOV-1997; 97US-0066511P.	
PR	24-NOV-1997; 97US-0066770P.	
PR	24-NOV-1997; 97US-0066772P.	
PR	25-NOV-1997; 97US-0066840P.	
XX		
PA	(GETH) GENENTECH INC.	
PI	Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;	
PI		
XX		
DR	N-PSDB; AAX52229.	
XX	New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.	
PT	Claim 12; Fig 32; 320pp; English.	
PS		
XX	AAY13344-403 represent secreted and transmembrane human proteins. The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO333 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract	
XX		
SQ	Sequence 398 AA;	
	Query Match 100.0%; Score 2086; DB 2; Length 398; Best Local Similarity 100.0%; Pred. No. 4.5e-149; Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSPWTSDTETVAGGTVLKCQVKDHEDSSL 60	
Db	1 MGAPAAASLLLLLLFACCCWAPGGANLSQDDSPWTSDTETVAGGTVLKCQVKDHEDSSL 60	
QY	61 QMSNPAQQOTLYFGKRALRDNRILQVTSTPHELSSISINVALADGEYTCSIFTMPVRTA 120	
Db	61 QMSNPAQQOTLYFGKRALRDNRILQVTSTPHELSSISINVALADGEYTCSIFTMPVRTA 120	
QY	121 KSLVTVLGIPQKIITGYKSSLREKDTATLNCQSGSKPAARLTWRKGDLHGEPTRIQ 180	
Db	121 KSLVTVLGIPQKIITGYKSSLREKDTATLNCQSGSKPAARLTWRKGDLHGEPTRIQ 180	
QY	181 EDPNGKTFTVSSSVTFQVTTREDGDGASIVCSNVHESLKCADRSTSQRILEVLTPTAMIRPD 240	
Db	181 EDPNGKTFTVSSSVTFQVTTREDGDGASIVCSNVHESLKCADRSTSQRILEVLTPTAMIRPD 240	
QY	241 PPHREGOKLLHCGRGNVPQOYLWEKEGSVPPLKMTQESALIFFPLNKSDSGTGCT 300	
Db	241 PPHREGOKLLHCGRGNVPQOYLWEKEGSVPPLKMTQESALIFFPLNKSDSGTGCT 300	
QY	301 ATSNMGSYKAYTYTLNVNDPSPVPSSSSTHYAIIGGIIVAFIVFLLLIMLIFLGHYLIHRKG 360	
Db	301 ATSNMGSYKAYTYTLNVNDPSPVPSSSSTHYAIIGGIIVAFIVFLLLIMLIFLGHYLIHRKG 360	
QY	361 TYLTHEAKGSDPADPADTAIINAEGGQGGDKKEYFI 398	
Db	361 TYLTHEAKGSDPADPADTAIINAEGGQGGDKKEYFI 398	

CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity or other activities. (Updated on 25-MAR-2003 to correct PR
 field.)
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLFFACCCWAPGANLSQDSDPWTSDVAGGVVLKQVKDHEDSSL 60
 DB LLLLLLLLLLLLLLFFACCCWAPGANLSQDSDPWTSDVAGGVVLKQVKDHEDSSL 60
 QY 61 QWSNPAQOTLYFGEKRALDNRILQVLTSTPHELSSISNVALADGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDNRILQVLTSTPHELSSISNVALADGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSQRIEVLVYTPMTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSQRIEVLVYTPMTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGQKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSYKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLRHKG 360
 DB 301 ATSNMGSYKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLRHKG 360
 QY 361 TYLTHEAKSGDDPADADTAIINAEQSGGDDKKKEYFI 398
 DB 361 TYLTHEAKSGDDPADADTAIINAEQSGGDDKKKEYFI 398
 RESULT 2
 ID AAY29592
 AC AAY29592 standard; protein; 398 AA.
 XX
 DT 14-OCT-1999 (first entry)
 XX Human MBGP1 protein.
 XX
 KW Human; MBGP1; therapy; diagnosis; immunoglobulin; multiple sclerosis;
 KW cancer; neuronal disorder; CNS disorder; developmental disorder;
 KW spinal injury; degenerative condition; viral infection; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN EP93124-A2.
 XX
 PD 01-SEP-1999.
 XX
 PF 27-OCT-1998; 98EP-00203617.
 XX
 PR 24-FEB-1998; 98GB-00003952.
 PR 12-AUG-1998; 98GB-00017588.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Duckworth DM, Burgess NA;
 XX
 DR WPI; 1999-480841/41.
 DR N-PSDB; AAZ08540.
 XX
 PT New immunoglobulin superfamily member, useful for diagnosing and treating

Pf multiple sclerosis and cancer.
 XX Claim 4; Page 17-18; 21pp; English.
 PS
 CC The present sequence represents human MBGP1, which is a member of the
 CC immunoglobulin superfamily. MBGP1 may be used to screen for its agonists
 CC or antagonists by contacting MBGP1 with the candidate compound and
 CC detecting any alteration in activity of MBGP1 or in a label attached to
 CC the candidate. Alternatively the effect of a candidate agonist or
 CC antagonist compound on the production of mRNA encoding MBGP1 may be
 CC detected using an ELISA assay. Diseases or conditions arising from
 CC altered expression or activity of MBGP1 may be diagnosed by detecting
 CC MBGP1 in a sample from a patient or detecting a mutation in the
 CC polynucleotide encoding MBGP1 (I) in the genome of a patient. These
 CC diseases or conditions include neuronal disorders such as multiple
 CC sclerosis, CNS disorders, developmental disorders, spinal injury,
 CC degenerative conditions, cancer and viral infections. Detection of (I)
 CC may be used for chromosome mapping and tissue localization. MBGP1 and (I)
 CC may be administered to patients as vaccines or as part of a gene therapy
 CC regime respectively, to treat the diseases and conditions listed above.
 CC Antibodies against MBGP1 may be used to isolate or identify clones
 CC expressing MBGP1 or to purify MBGP1 by affinity chromatography. MBGP1 may
 CC also be used to identify molecules which interact with it in or on the
 CC surface of cells. Antagonists of MBGP1 may be administered to patients
 CC suffering from the above diseases or conditions related to increased
 CC expression or activity of MBGP1. Agonists of MBGP1 may similarly be used
 CC in cases of diseases or conditions related to decreased expression or
 CC activity of MBGP1
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2086; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 4.5e-149;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGAPAAASLLLLLFFACCCWAPGANLSQDSDPWTSDVAGGVVLKQVKDHEDSSL 60
 DB 1 MGAPAAASLLLLLFFACCCWAPGANLSQDSDPWTSDVAGGVVLKQVKDHEDSSL 60
 QY 61 QWSNPAQOTLYFGEKRALDNRILQVLTSTPHELSSISNVALADGEYTCSTFTMPVRTA 120
 DB 61 QWSNPAQOTLYFGEKRALDNRILQVLTSTPHELSSISNVALADGEYTCSTFTMPVRTA 120
 QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
 QY 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSQRIEVLVYTPMTAMIRPD 240
 DB 181 EDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKGDADSTSQRIEVLVYTPMTAMIRPD 240
 QY 241 PPHREGQKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
 DB 241 PPHREGQKLLHCEGRGNPVPQQYLWEKEGSPVPLKMTQESALIFPFLNKSDSGTYGCT 300
 QY 301 ATSNMGSYKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLRHKG 360
 DB 301 ATSNMGSYKAYTYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLMLIFLGHYLRHKG 360
 QY 361 TYLTHEAKSGDDPADADTAIINAEQSGGDDKKKEYFI 398
 DB 361 TYLTHEAKSGDDPADADTAIINAEQSGGDDKKKEYFI 398
 RESULT 3
 ID AAY13358
 AC AAY13358 standard; protein; 398 AA.
 XX
 AC AAY13358;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of protein PRO258.

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 45.5528 Seconds
(without alignments)
2468.650 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPAAALLLLLLPACCA.....AIIAEGGQSGDDKKEYFI 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003s:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2086	100.0	398	2	AAW80405 A secrete
2	2086	100.0	398	2	AAY29592 Human MBG
3	2086	100.0	398	2	AAY13358 Amino aci
4	2086	100.0	398	3	AAY94403 Human ACA
5	2086	100.0	398	3	AAY69288 Amino aci
6	2086	100.0	398	3	AAY45095 Human LDC
7	2086	100.0	398	3	ADC78404 Human PRO
8	2086	100.0	398	4	AAB80226 Human PRO
9	2086	100.0	398	4	AAL12345 Human PRO
10	2086	100.0	398	4	AAB53083 Human PRO
11	2086	100.0	398	5	ABB84838 Human PRO
12	2086	100.0	398	5	ABB95444 Human arg
13	2086	100.0	398	5	ABP61823 Human pol
14	2086	100.0	398	6	ABU71604 Human PRO
15	2086	100.0	398	6	ABO17789 Novel hum
16	2086	100.0	398	6	ABU71459 Human PRO
17	2086	100.0	398	6	ABU81043 Human PRO
18	2086	100.0	398	6	ABU71905 Human sec
19	2086	100.0	398	6	ABO01788 Novel hum
20	2086	100.0	398	6	ABU66743 Human PRO
21	2086	100.0	398	6	ABU54361 Human sec
22	2086	100.0	398	6	ABO47376 Human sec
23	2086	100.0	398	6	ABU59824 Novel sec
24	2086	100.0	398	6	ABO25014 Human sec
25	2086	100.0	398	6	ABU64513 Human sec

26	2086	100.0	398	6	ABU67359 Human sec
27	2086	100.0	398	6	ABO14879 Human sec
28	2086	100.0	398	6	ABU67019 Human sec
29	2086	100.0	398	6	ABU69636 Novel hum
30	2086	100.0	398	6	ABO14818 Human sec
31	2086	100.0	398	6	ADA45867 Novel hum
32	2086	100.0	398	6	ADA76298 Human PRO
33	2086	100.0	398	6	ADB29289 Human sec
34	2086	100.0	398	6	ADA18948 Human PRO
35	2086	100.0	398	6	ADA61571 Homo sapi
36	2086	100.0	398	6	ADB19356 Novel hum
37	2086	100.0	398	6	ADB27897 Human PRO
38	2086	100.0	398	6	ADA86376 Novel hum
39	2086	100.0	398	6	ADB15940 Human PRO
40	2086	100.0	398	6	ADA47726 Human PRO
41	2086	100.0	398	6	ADA18145 Human sec
42	2086	100.0	398	6	ABO32770 Human sec
43	2086	100.0	398	6	ADA67521 Human PRO
44	2086	100.0	398	6	ADB30528 Human PRO
45	2036	100.0	398	6	ADA85824 Novel hum

ALIGNMENTS

RESULT 1

AAW80405

ID AAW80405 standard; protein; 398 AA.

XX AC AAW80405;

XX DT 25-MAR-2003 (revised)

DT 13-JAN-1999 (first entry)

XX DE A secreted protein encoded by clone cr1162_25.

XX KW Secreted protein; immune stimulating; suppressing;

KW haematopoiesis regulating activity; tissue growth activity; activin;

KW inhibin activity; chemotactic; chemokinetic activity; haemostatic;

KW thrombolytic activity; anti-inflammatory activity; cadherin;

KW tumour invasion suppressor activity; tumour inhibition activity.

XX OS Homo sapiens.

XX PN WO9844113-A1.

XX PD 08-OCT-1998.

XX PF 27-MAR-1998; 98WO-US006176.

XX PR 28-MAR-1997; 97US-00823330.

XX PR 25-MAR-1998; 98US-00047661.

XX PA (GEMY) GENETICS INST INC.

XX PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;

XX DR WPI: 1998-542703/46.

XX DR N-PSDB; AAV63189.

XX PT New isolated polynucleotide(s) and secreted proteins - are obtained from human cDNA libraries prepared from adult testes, foetal brain, adult brain, adult blood and placenta.

XX PS Claim 13; Page 70-71; 124pp; English.

XX CC The present sequence represents a secreted protein. The nucleic acid

CC sequence is isolated from a human adult testes cDNA library using probe AAV63200. The polypeptide may have biological activities such as e.g. nutritional activity, immune stimulating or suppressing activity,

CC haematopoiesis regulating activity, tissue growth activity, haemostatic activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

DR MGD; MGI:1889272; Igsf4.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:008021; C:synaptic vesicle; IDA.
DR GO; GO:0018347; F:calcium-independent cell adhesion molecule . . .; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0007416; P:synaptogenesis; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;

Query Match 35.3%; Score 736.5; DB 11; Length 445;
Best Local Similarity 38.4%; Pred. No. 1.4e-54;
Matches 163; Conservative 74; Mismatches 144; Indels 43; Gaps 8;

QY 9 LLLLLPACCAFGANLSODSQPWTSDETVAGGTVLKCOVKDHDSSSLQWSNPAQQ 68
DB 31 LLLLLISAAALIFTG-----DQNLFTKQTVIEGEVATISQVKNKSDSVIQLNPNRQ 85

QY 69 TLYFGEKRALRDNRIOLVTSHPHLSISISNVALADEGYTCSIFTMPVRTAKSLVTVLG 128
DB 86 TIVFRDPRPLKDSRFQLNPFSSSELKVSLSNVSISDEGRYFCQLYTDPPQESYTTITVLV 145

QY 129 IPQKPIITGYKSLREKDYATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKTF 188
DB 146 PPRNLMIDIQDFAVEGEIEVNCAMASKPATTIIRFKGNKELGK-SEVEEWS--MY 202

QY 189 TVSSSVTFQVTRDDGASIVCSVNHSKAGDRSTSORIEVLYTPTAMIRPDPP---HPR 245
DB 203 TVTSQLMLKVHKEDDGVVICQVEHPAVTG-NLQTRYLEVQYKQVHIQMTYFLOGLTR 261

QY 246 EGOKLLHCEGRGNPVPQQYLWEK-EGSVPLPKMTQESALIFPFLNKSDSGTYGCTATSN 304
DB 262 EGDAFELTCEAIGKQPQVVMVTVVRVDEMPQHAVLSGPNLFINNLKNTDNGTYRCEASNI 321

QY 305 MGSYKAYYTLNVNDPS---PVPSSSTY-----HAIIG 334
DB 322 VGKAHSDYMLYVDPTTIPPPPTTTTITTTTTSILTIITDSRAGEEGTIGAVDHAVIG 381

QY 335 GIVAFIVFLLLIMLIIFLGHYLIIRHKGYLTAEAKGSDPADADTAIINAEQGSGGDDKK 394
DB 382 GVAVVVVFAMCLLIILGRYFAHKGYTFTEAKGADDAADADTAIINAEQGQNNSEKK 441

QY 395 EYFI 398
DB 442 EYFI 445

Search completed: May 27, 2004, 09:34:58
Job time : 33.6383 secs

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK001560; BAA91756.1; --
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003598; Neurexin-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 163 AA; 17860 MW; FB746375A05B0006 CRC64;

Query Match 41.8%; Score 872; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 7.9e-67;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFPFLNKSDSG 295

Db 1 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFPFLNKSDSG 60

QY 296 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYL 355

Db 61 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYL 120

QY 356 IRHKGTYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 398

Db 121 IRHKGTYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 163

RESULT 13

Q8KJLH8 PRELIMINARY; PRT; 163 AA.

AC Q8KJLH8
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to hypothetical protein FLJ10698.
GN NECL1.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Retina;

RA Strausberg R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC029659; AAH29659.1; --

DR MGD; MGI:2137858; Necl1.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

KW Hypothetical protein; Immunoglobulin domain.

SQ SEQUENCE 163 AA; 17773 MW; 1DBA70A03B71BBA CRC64;

Query Match 39.8%; Score 831; DB 11; Length 163;
Best Local Similarity 95.1%; Pred. No. 2.6e-63;
Matches 155; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 236 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFPFLNKSDSG 295

Db 1 MIRPPPPHREGQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFPFLNKSDSG 60

QY 296 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYL 355

Db 61 TYGCTATSNMGSYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYL 120

QY 356 IRHKGTYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 398

Db 121 IRHKGTYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 163

Db 121 IRHKGTYLTHEAKGSDADPADTAIINAEQSGGDDKKEYFI 163

RESULT 14

Q8BSQ8 PRELIMINARY; PRT; 152 AA.

AC Q8BSQ8
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Nectin-like 1 (Fragment).
GN NECL1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Body;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs";

RL Nature 420:563-573 (2002).

DR EMBL; AK030782; BAC27137.1; --

DR MGD; MGI:2137858; Necl1.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00408; IGC2; 1.

DR PROSITE; PS50835; IG-LIKE; 1.

FT NON TER 1

SQ SEQUENCE 152 AA; 16458 MW; E41F6BAD6A413A7 CRC64;

Query Match 37.2%; Score 777; DB 11; Length 152;

Best Local Similarity 96.1%; Pred. No. 1e-56;

Matches 146; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 247 GQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFPFLNKSDGTATSNMG 306

Db 1 GQKLLHCEGRNPVPOQYLWEKGSVPPLKWTQESALIFPFLNKSDGTATSNMG 60

QY 307 SYKAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHE 366

Db 61 SYTAYITLVNDPSPVSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHE 120

QY 367 AKGSDADPADTAIINAEQSGGDDKKEYFI 398

Db 121 AKGSDADPADTAIINAEQSGGDDKKEYFI 152

RESULT 15

Q8K3T6 PRELIMINARY; PRT; 445 AA.

AC Q8K3T6
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Synaptic cell adhesion molecule 1.
GN IGSF4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL;

RA Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,

RA Sudhof T.C.;

RT "SynCAM, a synaptic adhesion molecule that drives synapse assembly.;"

RL Science 0:0-0(2002).

DR EMBL; AF539424; AAN01614.1; --

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AC Q8N3J6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKF2P761G128.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue: Amygdala;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834270; CAD38945.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG. 3.
DR SMART; SM00409; IG. 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein, Immunoglobulin domain.
SQ SEQUENCE 435 AA; 47554 MW; 59DDDD41B7F34D446 CRC64;

Query Match 48.6%; Score 1014; DB 4; Length 435;
Best Local Similarity 47.2%; Pred. No. 2.1e-78;
Matches 204; Conservative 73; Mismatches 107; Indels 48; Gaps 6;

QY 11 LLLLFACWAPGANLSQDSQ--PWTSDETVVAGGVVLKQVKHEDSSLOWNSPAQOT 69
DB 8 VLFYFVC---GLLQSGQGQFPFLQNTVTVVEGGTAILTCRVDQNDNTSLOWNSPAQOT 63
QY 70 LYFGEKRALDRNIQLVSTPHLSISGNVALADGEYTCSTFTMPVTKSLVTLGI 129
DB 64 LVPDDKKALDRNRIELVRASWHELSISVDSVLSDEGQYTCSTFTMPVTKSKAYLTVLGV 123
QY 130 PKPIITIGYKSSIREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKTTT 189
DB 124 PEKPIQSGFSSPWEGLMQLTCKTSGSKPAADIRWFKNDEIKDKVYLKEEDANKTTT 183
QY 190 VSSVTFQVTRDDGASIVCSNVHSLKGADRTSQRIEVLVYPTAMIRPDPPHREGQK 249
DB 184 VVSTLDFRDRSDGVAVICRVDPHESLNATPVAMQVLEIHYTPSVKIIIPSTFPFQEQP 243
QY 250 LILHCEGRGNPVPQQYLWEKESV---PPLKMTQESALIPFPFNKSDSGTYGCTATSNMG 306
DB 244 LIILCESKGLPEPVLWTKDGGELPDPDRMVVSGRELNLFLNKTDNGTYRCEATNTIG 303
QY 307 SYKAYTYTLNVND-----PSPV-----PSSSSTY----- 329
DB 304 QSSAEYVLIHVDVENTLPTIIPSLTATVTTVAITTSPTTSATTSSIRDNPALAGQN 363
QY 330 ---HAITGGIVAFVFLLLMLPLGHLRHKGYTLTHEAKGSDADPADDTALINAEKG 386
DB 364 GPDHALIGGIVAVVVFVTLCSIFLLGRLYLRHKGYTLTHEAKGAEADPADDTALINAEGS 423
QY 387 QSGGDDKKKEYFI 398
DB 424 QVNAEKKKEYFI 435

RESULT 11
Q8IZP8 ID Q8IZP8 PRELIMINARY; PRT; 437 AA.
AC Q8IZP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like protein 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
AF538973; AANI6388.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_c2.
Pfam; PF00047; IG. 3.
SMART; SM00409; IG. 2.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 437 AA; 47593 MW; D23DB347F5E5F023 CRC64;

Query Match 48.6%; Score 1013.5; DB 4; Length 437;
Best Local Similarity 47.1%; Pred. No. 2.3e-78;
Matches 206; Conservative 75; Mismatches 107; Indels 49; Gaps 7;

QY 11 LLLLFAC--CWAPGANLSQ--DDSQ---PWTSDETVVAGGVVLKQVKHEDSSLOWNS 64
DB 1 MEVFLCLNLSLVPAASAKNKKVKGSGQGFPLQNTVTVVEGGTAILTCRVDQNDNTSLOWNS 60
QY 65 PAQOTLYFGEKRALDRNIQLVSTPHLSISGNVALADGEYTCSTFTMPVTKSLV 124
DB 61 PAQOTLYFDDKKALDRNRIELVRASWHELSISVDSVLSDEGQYTCSTFTMPVTKSKAYL 120
QY 125 TVLGIPIQPIITIGYKSSIREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPN 184
DB 121 TVLGVPEKPIQSGFSSPWEGLMQLTCKTSGSKPAADIRWFKNDEIKDKVYLKEDAN 180
QY 185 GKTFTVSSVTFQVTRDDGASIVCSNVHSLKGADRTSQRIEVLVYPTAMIRPDPPH 244
DB 181 RKTFTVSSVTLDFRDRSDGVAVICRVDPHESLNATPVAMQVLEIHYTPSVKIIIPSTFP 240
QY 245 REGQKLLHCEGRGNPVPQQYLWEKESV---PPLKMTQESALIPFPFNKSDSGTYGCTA 301
DB 241 QEGQPLIITCESKGLPEPVLWTKDGGELPDPDRMVVSGRELNLFLNKTDNGTYRCEA 300
QY 302 TSNMGSYKAYTYTLNVND-----PSPV-----PSSSSTY----- 329
DB 301 TWITQSSAEYVLIHVDVENTLPTIIPSLTATVTTVAITTSPTTSATTSSIRDNPNA 360
QY 330 -----HAITGGIVAFVFLLLMLPLGHLRHKGYTLTHEAKGSDADPADDTAL 381
DB 361 LAGQNGPDHALIGGIVAVVVFVTLCSIFLLGRLYLRHKGYTLTHEAKGAEADPADDTAI 420
QY 382 NAEGGQSGDDKKKEYFI 398
DB 421 NAEGGQVNAEKKKEYFI 437

RESULT 12
Q9NVJ5 ID Q9NVJ5 PRELIMINARY; PRT; 163 AA.
AC Q9NVJ5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ10698.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoaka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuko Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
```

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Db 304 QSSAEYVLIVHDPNSLAGQDPHALIGGIVAVVVFVTLCSIFLLGRYLARHKGYLTNE 363
QY 367 AKGSDADPADTATINAEAGQSGGDDKKEYFI 398
Db 364 AKGAEDAPDADTATINAEAGSQVNAEEKKEYFI 395
RESULT 8
Q8BYP1 PRELIMINARY; PRT; 404 AA.
AC Q8BYP1;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK038842; BAC30148.1; -.
DR MGD; MGI:2442722; A830029E02RIK.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 404 AA; 44387 MW; E9C84191AA687473 CRC64;
Query Match 49.7%; Score 1037.5; DB 11; Length 404;
Best Local Similarity 53.1%; Pred. No. 1.8e-80;
Matches 196; Conservative 68; Mismatches 102; Indels 3; Gaps 1;
QY 33 PWTSDTVVAGGVTLVKCOVKDHESSLOWNSPAQOTLYFGEKRALRDNRILQVSTPHE 92
Db 36 PLTQNVTVVEGGTALTCTCRVDQNDNTSLQWNSPAQOTLYFDDKKALRDNRILVRSWHE 95
QY 93 LSISISNALADEGYTCSTFTMPVTKSLVTLGIPQKPIITGYKSSLRKDTATLNC 152
Db 96 LSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGSPVMEGDLMLQTC 155
QY 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKTFVTSSTVFTVTRDDGASIVCSVN 212
Db 156 KTSGSKPAADIRFWKNDKEIKDKYLKEEDANRKTFTVSTLDFRVDSDGVAVICRVD 215
QY 213 HESLGADSTSRIVLYTPTAMIRPDPPHREGQKLLHCEGRNPVPQVYLWEKGS 272
Db 216 HESLNATPQVAMQVLEIHYTPSKVLIPTFPFQEGQALTCTCSKGKPLPEPVLWTKGA 275
QY 273 V---PPLKMTQESALIFPFLNKSDSGTYGCTATNMGSKYKAYVTLNVNDPSPVSSSTY 329
Db 276 ELPPDPRMVVSGRELNIFLUNKTDNGTYRCAKNTIGQSSAEYVLIVHDPNSLAGQNGPD 335
QY 330 HALIGGIVAFIVFLLIMLIFLGHYLRHKGYLTNEAGSDPADPADTATINAEAGQSG 389
Db 336 HALIGGIVAVVVFVTLCSIFLLGRYLARHKGYLTNEAGSDPADPADTATINAEAGSQVN 395
QY 390 GDDKKEYFI 398
Db 396 AEEKKEYFI 404
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RESULT 10
Q8N3J6 PRELIMINARY; PRT; 435 AA.
ID Q8N3J6
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RESULT 9
Q8BLQ9 PRELIMINARY; PRT; 404 AA.
AC Q8BLQ9;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DE Weakly similar to BK134P22.1.
GN A830029E02RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK043760; BAC31646.1; -.
DR MGD; MGI:2442722; A830029E02RIK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; IG_3.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 404 AA; 44388 MW; 091E493B82CAFE5B CRC64;
Query Match 49.7%; Score 1037.5; DB 11; Length 404;
Best Local Similarity 53.1%; Pred. No. 1.8e-80;
Matches 196; Conservative 68; Mismatches 102; Indels 3; Gaps 1;
QY 33 PWTSDTVVAGGVTLVKCOVKDHESSLOWNSPAQOTLYFGEKRALRDNRILQVSTPHE 92
Db 36 PLTQNVTVVEGGTALTCTCRVDQNDNTSLQWNSPAQOTLYFDDKKALRDNRILVRSWHE 95
QY 93 LSISISNALADEGYTCSTFTMPVTKSLVTLGIPQKPIITGYKSSLRKDTATLNC 152
Db 96 LSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGSPVMEGDLMLQTC 155
QY 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKTFVTSSTVFTVTRDDGASIVCSVN 212
Db 156 KTSGSKPAADIRFWKNDKEIKDKYLKEEDANRKTFTVSTLDFRVDSDGVAVICRVD 215
QY 213 HESLGADSTSRIVLYTPTAMIRPDPPHREGQKLLHCEGRNPVPQVYLWEKGS 272
Db 216 HESLNATPQVAMQVLEIHYTPSKVLIPTFPFQEGQALTCTCSKGKPLPEPVLWTKGA 275
QY 273 V---PPLKMTQESALIFPFLNKSDSGTYGCTATNMGSKYKAYVTLNVNDPSPVSSSTY 329
Db 276 ELPPDPRMVVSGRELNIFLUNKTDNGTYRCAKNTIGQSSAEYVLIVHDPNSLAGQNGPD 335
QY 330 HALIGGIVAFIVFLLIMLIFLGHYLRHKGYLTNEAGSDPADPADTATINAEAGQSG 389
Db 336 HALIGGIVAVVVFVTLCSIFLLGRYLARHKGYLTNEAGSDPADPADTATINAEAGSQVN 395
QY 390 GDDKKEYFI 398
Db 396 AEEKKEYFI 404
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QY 121 KSLVTLGIPQPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
 DB 121 KSLVTLGIPQPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQ 180
 QY 181 EDPNGKTFVTSSSVTFQVTRDDGASIVCSNVHESLKGADRSQTSQRIEVLVYPTTAMIRPD 240
 DB 181 EDPND-----TPTAMIRPD 194
 QY 241 PPHREGQKLLHCBGRGNPVPQOVLWEKESGVPPLKMTQ 280
 DB 195 PPHREGQKLLHCBGRGNPVPQOVLWEKESGVPPLKMTQ 234

RESULT 6
 Q8BZP4 PRELIMINARY; PRT; 395 AA.
 ID Q8BZP4;
 AC Q8BZP4;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Weakly similar to BK134P22.1.
 GN A830029E02RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK033973; BAC28533.1; -.
 DR MGD; MGI:2442722; A830029E02RIK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016337; P:cell-cell adhesion; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG.c2.
 DR InterPro; IPR003989; VCAM-1.
 DR Pfam; PF00047; IG.3.
 DR PRINTS; PR01474; VCAM1.
 DR SMART; SM00409; IG.2.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 SQ SEQUENCE 395 AA; 43516 MW; EB70FB5363D872F3 CRC64;

Query Match 49.8%; Score 1039; DB 11; Length 395;
 Best Local Similarity 51.3%; Pred. No. 1.3e-80;
 Matches 201; Conservative 71; Mismatches 112; Indels 8; Gaps 3;
 QY 11 LLLFACWAPGAGNLSQDSDQ-PWTSDETVVAGTVVLKCVKDHEDSSLOWNSPAQQT 69
 DB 8 VLRFYSVC-----GLLQSGSQGFPLTQNTVTVVEGTAITLCRVQDNDNTSLQNSPAQQT 63
 QY 70 LYFGEKRALDRNRILQVLTSTPHELISISINVALADEGETCSIFTPVPTAKSLVTLGI 129
 DB 64 LYFDDKALDRNRILVRASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGV 123
 QY 130 POKPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQEDPNKTKFT 189
 DB 124 PEKQISGSPSPVMEGLMQLTCKTSSGKPAADIRWFKNDEIKDVYKLEEADNRKTKFT 183
 QY 190 VSSSVTFQVTRDDGASIVCSNVHESLKGADRSQTSQRIEVLVYPTTAMIRPDPPHREGQK 249
 DB 184 VSSLDFVRDSDGVAICRVDSHESLNATPQVAMQVLEIHYTPSVKIIIPSTPPQEGQA 243
 QY 250 LLLHCBGRGNPVPQOVLWEKESV---PPLKMTQESALIPFPLNKSDSGTYGCTATSNMG 306
 DB 244 LTLTCSKGKPLPEPVLTKDGAELPDRMVMVSGRELNLFLNKTNDNGTYRCEATNTIG 303

QY 307 SYKAYTILNVNDPSPVPSSSTYHAIIGGIIVAFIVFLLIMLIFLGHYLRHKGTYLTHE 366
 DB 304 QSSAKYVLIVHDPNSLAGQCPDHALIGGIIVAVVVFVTLCSIFLLGRYLARKHGYLTNE 363
 QY 367 AKGSDDAPDADTAIINAEAGGSGGDDKKEYFI 398
 DB 364 AKGAEDAPDADTAIINAEAGSQVNAEKEKEYFI 395

RESULT 7
 Q8BXJ7 PRELIMINARY; PRT; 395 AA.
 ID Q8BXJ7;
 AC Q8BXJ7;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Weakly similar to BK134P22.1.
 GN A830029E02RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK046800; BAC32876.1; -.
 DR MGD; MGI:2442722; A830029E02RIK.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016337; P:cell-cell adhesion; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG.c2.
 DR InterPro; IPR003989; VCAM-1.
 DR Pfam; PF00047; IG.3.
 DR PRINTS; PR01474; VCAM1.
 DR SMART; SM00409; IG.2.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 SQ SEQUENCE 395 AA; 43517 MW; E57E1BBD6D3672F9 CRC64;

Query Match 49.8%; Score 1039; DB 11; Length 395;
 Best Local Similarity 51.3%; Pred. No. 1.3e-80;
 Matches 201; Conservative 71; Mismatches 112; Indels 8; Gaps 3;
 QY 11 LLLFACWAPGAGNLSQDSDQ-PWTSDETVVAGTVVLKCVKDHEDSSLOWNSPAQQT 69
 DB 8 VLRFYSVC-----GLLQSGSQGFPLTQNTVTVVEGTAITLCRVQDNDNTSLQNSPAQQT 63
 QY 70 LYFGEKRALDRNRILQVLTSTPHELISISINVALADEGETCSIFTPVPTAKSLVTLGI 129
 DB 64 LYFDDKALDRNRILVRASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGV 123
 QY 130 POKPIITGYKSSLRKXDTATLNCSSGSKPAARLTWRKGDQELHGPTRIQEDPNKTKFT 189
 DB 124 PEKQISGSPSPVMEGLMQLTCKTSSGKPAADIRWFKNDEIKDVYKLEEADNRKTKFT 183
 QY 190 VSSSVTFQVTRDDGASIVCSNVHESLKGADRSQTSQRIEVLVYPTTAMIRPDPPHREGQK 249
 DB 184 VSSLDFVRDSDGVAICRVDSHESLNATPQVAMQVLEIHYTPSVKIIIPSTPPQEGQA 243
 QY 250 LLLHCBGRGNPVPQOVLWEKESV---PPLKMTQESALIPFPLNKSDSGTYGCTATSNMG 306
 DB 244 LTLTCSKGKPLPEPVLTKDGAELPDRMVMVSGRELNLFLNKTNDNGTYRCEATNTIG 303
 QY 307 SYKAYTILNVNDPSPVPSSSTYHAIIGGIIVAFIVFLLIMLIFLGHYLRHKGTYLTHE 366

SEQUENCE 394 AA: 42730 MW: F1141D8E6B69254A CRC64:

```

DR SMART: SM00408; IGC2: 3.
DR PROSITE; P550835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Signal.
FT SIGNAL 1 24 POTENTIAL.
SQ SEQUENCE 398 AA; 43300 MW; 601B2FB5D512DB6C CRC64;

Query Match
Best Local Similarity 100.0%; Score 2086; DB 4; Length 398;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
POTENTIAL.

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDSSQPWTSDETVVAGGTIVLKQVKDHEDSSL 60
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQDSSQPWTSDETVVAGGTIVLKQVKDHEDSSL 60
QY 61 QWSNPAQQTLYGEGKALRDNRIQLVTSIPHELSSISINVALADEGEYTCSTFTMPVRTA 120
DB 61 QWSNPAQQTLYGEGKALRDNRIQLVTSIPHELSSISINVALADEGEYTCSTFTMPVRTA 120
QY 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
DB 121 KSLVTVLGIPQKPIITGYKSSLRKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ 180
QY 181 EDPNGKFTVSSSVTPQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTTAMIRPD 240
DB 181 EDPNGKFTVSSSVTPQVTRDDGASIVCSVNHESLKGADRTSQRIEVLVYPTTAMIRPD 240
QY 241 PPHREGQKLLHCEGRGNPVPQOYLWEKEGSPVPLKMTQESALIPFPLNKSDSGTYGCT 300
DB 241 PPHREGQKLLHCEGRGNPVPQOYLWEKEGSPVPLKMTQESALIPFPLNKSDSGTYGCT 300
QY 301 ATSNMGSYKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
DB 301 ATSNMGSYKAYTYTLNVNDSPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLRHKG 360
QY 361 TYLTAEKSGDDPADDTAIINAEQSGGDDKKEYFI 398
DB 361 TYLTAEKSGDDPADDTAIINAEQSGGDDKKEYFI 398

RESULT 2
Q9UJF1 PRELIMINARY; PRT; 432 AA.
AC Q9UJF1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE BK134P22.1 (Novel protein similar to mouse IMMUNOSUPERFAMILY protein BL2) (NECTIN-like protein 1).
DE BK134P22.1 OR NECL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou Y., Du G., Yuan J., Qiang B.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035403; CAB56227.1; -.
DR EMBL; AF062733; AAD17540.2; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003585; Neurexin-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00294; 4.1m; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; P550835; IG LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 432 AA; 47020 MW; AC474EFEC4C518C CRC64;

Query Match
Best Local Similarity 98.7%; Score 2059; DB 4; Length 432;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAASLLLLLLFACCAWPGGANLSQDSSQPWTSDETVVAGGTIVLKQVKDHEDSSL 29
DB 1 MGAPAAASLLLLLLFACCAWPGGANLSQDSSQPWTSDETVVAGGTIVLKQVKDHEDSSL 60
QY 30 ---DSQPWTSDETVVAGGTIVLKQVKDHEDSSQWNPAAQQTLYGEGKALRDNRIQLV 86
DB 61 ASQDSQPWTSDETVVAGGTIVLKQVKDHEDSSQWNPAAQQTLYGEGKALRDNRIQLV 120
QY 87 TSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLVTLGIPQKPIITGYKSSLRK 146
DB 121 TSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLVTLGIPQKPIITGYKSSLRK 180
QY 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTPQVTRDDGAS 206
DB 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTPQVTRDDGAS 240
QY 207 IVCSVNHESLKGADRTSQRIEVLVYPTTAMIRPDPPHREGQKLLHCEGRGNPVPQOYL 266
DB 241 IVCSVNHESLKGADRTSQRIEVLVYPTTAMIRPDPPHREGQKLLHCEGRGNPVPQOYL 300
QY 267 WEKEGSPVPLKMTQESALIPFPLNKSDSGTYGCTATSNMGSYKAYTYTLNVNDSPVSS 326
DB 301 WEKEGSPVPLKMTQESALIPFPLNKSDSGTYGCTATSNMGSYKAYTYTLNVNDSPVSS 360
QY 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTAEKSGDDPADDTAIINAE 386
DB 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTAEKSGDDPADDTAIINAE 420
QY 387 QSGGDDKKEYFI 398
DB 421 QSGGDDKKEYFI 432

RESULT 3
Q99N28 PRELIMINARY; PRT; 396 AA.
AC Q99N28
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin-like protein 1 (Membrane glycoprotein) (Nectin-like 1).
GN NECL1 OR TSL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y., Huang X., Yuan J., Qiang B.;
RT "Cloning and expression analysis of novel mouse cDNA encoding a membrane protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Fukami T., Maruyama T., Murakami Y.;
RL "Identification of a murine ortholog of the TSLC1-like gene 1.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA "Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573 (2002).";
RL Nature 420:563-573 (2002).
DR EMBL; AF195662; AAG35584.1; -.
DR EMBL; AY059393; AAL29691.1; -.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 32.6383 Seconds
(without alignments)

3847.506 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPASLALLLLFACWA.....AIIAEGSQSGGDKKEYFI 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mnc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	398	4 Q8N126	Q8N126 homo sapien
2	2059	98.7	432	4 Q9UJP1	Q9UJP1 homo sapien
3	1970	94.4	396	11 Q9N28	Q9N28 mus musculus
4	1282.5	61.5	394	13 Q7ZXX1	Q7ZXX1 xenopus lae
5	1203	57.7	234	4 Q81ZQ9	Q81ZQ9 homo sapien
6	1039	49.8	395	11 Q8BZP4	Q8BZP4 mus musculus
7	1039	49.8	395	11 Q8BXJ7	Q8BXJ7 mus musculus
8	1037.5	49.7	404	11 Q8BYP1	Q8BYP1 mus musculus
9	1037.5	49.7	404	11 Q8BLQ9	Q8BLQ9 mus musculus
10	1014	48.6	435	4 Q8N336	Q8N336 homo sapien
11	1013.5	48.6	437	4 Q81ZP8	Q81ZP8 homo sapien
12	872	41.8	163	4 Q9NVJ5	Q9NVJ5 homo sapien
13	831	39.8	163	11 Q8K1H8	Q8K1H8 mus musculus
14	777	37.2	152	11 Q8BSQ8	Q8BSQ8 mus musculus
15	736.5	35.3	445	11 Q8K3T6	Q8K3T6 mus musculus
16	736.5	35.3	445	11 Q8R4L1	Q8R4L1 mus musculus

17	736	35.3	442	4 Q9BY67	Q9BY67 homo sapien
18	727.5	34.9	417	11 Q7TNL1	Q7TNL1 mus musculus
19	726	34.8	456	11 Q8R5M8	Q8R5M8 mus musculus
20	724.5	34.7	443	4 Q8N2F4	Q8N2F4 homo sapien
21	607	29.1	388	4 Q8NFZ8	Q8NFZ8 homo sapien
22	598	28.7	388	11 Q8R464	Q8R464 mus musculus
23	573.5	27.5	381	4 Q9Y4A4	Q9Y4A4 homo sapien
24	514	24.6	295	11 Q9QYL6	Q9QYL6 mus musculus
25	510	24.4	295	11 Q9Z2H8	Q9Z2H8 mus musculus
26	508.5	24.4	306	11 Q9QYL4	Q9QYL4 mus musculus
27	503.5	24.1	278	11 Q9QYL3	Q9QYL3 mus musculus
28	499	23.9	289	11 Q9QYL5	Q9QYL5 mus musculus
29	474	22.7	333	4 Q86WB8	Q86WB8 homo sapien
30	471.5	22.6	336	11 Q9D6E7	Q9D6E7 mus musculus
31	471.5	22.6	336	11 Q80VG4	Q80VG4 mus musculus
32	345.5	16.6	403	6 Q8HY15	Q8HY15 lemur catta
33	307	14.7	412	6 Q8HY14	Q8HY14 cryptotagus
34	290	13.9	401	6 Q88835	Q88835 cercopithec
35	281	13.5	417	4 Q96BJ1	Q96BJ1 homo sapien
36	273	13.1	612	11 Q8BGQ5	Q8BGQ5 mus musculus
37	273	13.1	766	11 Q81OH3	Q81OH3 mus musculus
38	273	13.1	778	11 Q8BR86	Q8BR86 mus musculus
39	271	13.0	778	4 Q8IZU9	Q8IZU9 homo sapien
40	271	13.0	779	4 Q96JG0	Q96JG0 homo sapien
41	258.5	12.4	439	13 Q57349	Q57349 gallus gall
42	254	12.2	412	11 Q63611	Q63611 rattus norv
43	254	12.2	412	11 Q9R1E1	Q9R1E1 rattus norv
44	252.5	12.1	393	4 Q95727	Q95727 homo sapien
45	252	12.1	350	7 Q02869	Q02869 gallus gall

ALIGNMENTS

RESULT 1

Q8N126 Q8N126 PRELIMINARY; PRT; 398 AA.
AC Q8N126;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Brain immunoglobulin receptor precursor (Nectin-like protein 1)
DE (TSLC1-like 1).
GN TSLC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Cunningham S.A., Tran T.M., Arrate M.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RT "Isolation of the TSL1 and TSL2 genes, members of the tumor suppressor TSLC1 gene family encoding transmembrane proteins.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY046418; AAL02143.1; -
DR EMBL; BC033819; AAL02143.1; -
DR EMBL; BC033819; AAL02143.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.

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FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 354 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 258 258 N->S.
/FTIG=VAR_003907.
M->T.
/FTID=VAR_003908.

FT VARIANT 301 301
FT STRAND 32 33
FT STRAND 39 44
FT STRAND 52 59
FT TURN 61 62
FT STRAND 65 71
FT STRAND 76 78
FT TURN 84 85
FT STRAND 86 90
FT STRAND 95 100
FT STRAND 110 117
FT TURN 118 119
FT STRAND 120 123
FT STRAND 127 128
FT STRAND 130 131
SQ SEQUENCE 583 AA; 65132 MW; E023FB3974A60284 CRC64;

Query Match 10.8%; Score 225.5; DB 1; Length 583;
Best Local Similarity 22.4%; Pred. No. 7.8e-09;
Matches 80; Conservative 70; Mismatches 148; Indels 59; Gaps 14;

QY 2 GAPAASILLLLFACCAWAPGGANLSQDDSQPTSDFTVAGTIVLKCQVK-----53
Db 5 GASSCRLLFCLLISATVFRPG-----LGWYTVNSAY-GDTIIIPCRLDVPQNLMSG 54
QY 54 -----DHEDSS---LQSNPAQOTLYFGEKALRDNRILQVTSTPHELSTISINVALADEG 106
Db 55 KWKYKPDGSPVFIAPRSSTKSKVQDDVPEYKD-RLNL-----SENYTSLISNARISDEK 109
QY 107 EYTCISFTMP-VRTAKSLVTLVGLIPQKPIITGYKSSLRKXDATL-NCQSSGSKPAARLT 164
Db 110 RFVCMVLVEDNVFEAPTIVKVFQKPSKPEIVSKALFLETEQLKXGDCISEDSYPDGNIT 169
QY 165 WRKGDQBLH---GEPTRI---QEDPNGKFTVSSSVTFQVTRDDGASIVCSVNHESLKG 218
Db 170 WYRNGKVLHLEGNVLIIFKEMDPVTLQYTMSTLEYKTKADIQMPFTCSVTYYGPSG 229
QY 219 ADR-STSQRIEVIYTPAMIR-----PDPPHREGQKLLHCEGRGNVPQOYLWEKEGSV 273
Db 230 QKTIHSEQAVFDIYYTEQVTIQLVPEKNAIKEGDNITLKLGNNGNPPBEFLFYLPQGP 289
QY 274 PPLKMTQESALIFPFLNKSDDSGTYGCTATSNMGSYKAYITLVNDPSPVSSSTYH 330
Db 290 EGIRSSNTYTLN--DVRNATGDKCSU-----IDKSMIASTAITVH 330

Search completed: May 27, 2004, 09:35:46
Job time : 9.4531 secs
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FT SITE 432 435 SH2-BINDING (POTENTIAL) .
FT SITE 441 446 SH3-BINDING (POTENTIAL) .
FT SITE 455 458 SH2-BINDING (POTENTIAL) .
FT SITE 472 475 SH2-BINDING (POTENTIAL) .
FT SITE 498 501 SH2-BINDING (POTENTIAL) .
FT MOD_RES 431 431 PHOSPHORYLATION (BY TYR-KINASES)
(POTENTIAL) .
FT MOD_RES 455 455 PHOSPHORYLATION (BY TYR-KINASES)
(POTENTIAL) .
FT MOD_RES 472 472 PHOSPHORYLATION (BY TYR-KINASES) (BY
SIMILARITY) .
FT MOD_RES 498 498 PHOSPHORYLATION (BY TYR-KINASES) (BY
SIMILARITY) .
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 204 204 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 311 311 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL) .
FT VARIANT 23 23 N -> S.
FT VARIANT 28 28 T -> A.
FT VARIANT 61 61 S -> L.
FT VARIANT 70 70 K -> R.
FT VARIANT 120 120 Y -> H.
FT VARIANT 125 125 R -> Q.
FT VARIANT 127 127 E -> G.
FT VARIANT 129 129 R -> H.
FT VARIANT 132 132 M -> V.
FT VARIANT 145 145 S -> N.
FT VARIANT 153 153 L -> V.
FT VARIANT 203 203 N -> D.
FT VARIANT 261 261 G -> R.
FT VARIANT 302 302 F -> L.
FT VARIANT 316 316 F -> L.
FT VARIANT 337 337 G -> R.
FT VARIANT 367 367 S -> N.
FT VARIANT 422 422 Q -> L.
FT VARIANT 429 429 I -> F.
FT VARIANT 433 433 D -> E.
SQ SEQUENCE 506 AA; 55093 MW; 6B7E310677FCF9CB CRC64;
Query Match 10.9%; Score 226.5; DB 1; Length 506;
Best Local Similarity 23.1%; Pred. No. 5.5e-09;
Matches 98; Conservative 69; Mismatches 184; Indels 73; Gaps 18;
Qy 8 LLLLLL FACWAGGANLSODSOPWTSDETVVAGGVVLKCOVKDHD--SSLOW--S 63
Db 14 LCLLLAASNAWTGTAGDELQVTPERS-VSVAAGETATLHCTVLSLSPGVPIKFKGT 72
Qy 64 NPAQITLYFGEKRALDRNRIQLVSTPH--ELSGISINVALADEGEYTCISFTMPVRTA 120
Db 73 GPGEFIY-SQKEAPFRFTVNSDATKRNNDFFSIRISNITPADGVYCVKPKKEERGD 131
Qy 121 KSL-----VTVIGIPQKPIITGYKSLRKBKDTATLNCQSSGSKPA-ARLTWRKQDQEL 172
Db 132 MEFKSGPGTHLTVSAKPPVLSGPTVRATPEQTVFTCTSHGFSRPNISLKWFKNGNEL 191
Qy 173 HGEPTRIQEDNGKFTFTVSSVTVQVREDDGASIVCSVNHESLKGAD--RSTSORLEV 230
Db 192 SASQTSQVDPEDNNVSYISNSTKVLATGVDVHVSQVCEVAHVTLQGGPPLRGTLANLSETI 251
Qy 231 YTPATAMIRPDPPHREGQKLLHCE-GRGNFVPQOYLWEKEGSPPLKWTQESALIFPFL 289
Db 252 RVPPTL--EITGSPAGQNVNVCQVNFYRHLQLTLWLENGM-----SRTEASVFFV-- 303
Qy 290 NKDSGSGTYGCTATSNMGS-----YKAYYTLNVNDP-----SP 321

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Db 304 -ENKDGTFNQTSWFLVNSSAHREAVLTCQVHDGQPAVSKNHTLEVSAPQKDOTQOTP 362
Qy 322 VPSSS--STYHAIGGIVAFIVFILLIMLIFLGHVLIHKGTYLTHEAKGSDDA-----P 374
Db 363 GFNSDNWTSIFIVGVVWCALLVALLAAL-----YLLRIR-----QNKARGSTSTRLHP 413
Qy 375 DADT 378
Db 414 EKNT 417

RESULT 14
LAMP RAT STANDARD; PRT; 338 AA.
ID LAMP RAT
AC O62813.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Limbic system-associated membrane protein precursor (LSAMP) .
GN LSAMP OR LAMP.
OS Rattus norvegicus (Rat) .
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 29-49.
RC TISSUE=Hippocampus;
RX MEDLINE=95374785; PubMed=7646886;
RA Fimenta A.F., Zhukareva V., Barbe M.F., Reinoso B.S., Grimley C.,
RA Hensel W., Fischer I., Levitt P.;
RT "The limbic system-associated membrane protein is an Ig superfamily
RT member that mediates selective neuronal growth and axon targeting.";
RL Neuron 15:287-297(1995).
CC -!- FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING.
CC CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF
CC MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTH
CC OF THE HIPPOCAMPAL MOSSY FIBER PROJECTION.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: Expressed mostly by neurons comprising limbic-
CC associated cortical and subcortical regions that function in
CC cognition, emotion, memory, and learning.
CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS
CC DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE
CC THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN
CC HYPOTHALAMUS, PERIRHINAL CORTEX, AMYGDALA AND MEDIAL THALAMIC
CC REGION.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U31554; AAA86120.1; -.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003598; Ig_c2.
CC Pfam: PF00047; Ig; 3.
CC SMART: SM00408; IGC2; 2.
CC PROSITE: PS50835; IGLIKE; 3.
CC Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 28
FT CHAIN 29 315 LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROPEP 316 338 REMOVED IN MATURE FORM (POTENTIAL) .
FT DOMAIN 29 122 IG-LIKE C2-TYPE 1.
FT DOMAIN 132 214 IG-LIKE C2-TYPE 2.

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FT DOMAIN 376 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 436 442 POLY-GLU.
FT DOMAIN 443 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 138 138 L -> P (IN REF. 1).
FT CONFLICT 165 165 N -> D (IN REF. 1).
FT CONFLICT 342 342 P -> PP (IN REF. 2).
FT CONFLICT 428 428 S -> G (IN REF. 3).
SQ SEQUENCE 515 AA; 57064 MW; PFF608EB5FFB7A0F CRC64;

Query Match 11.0%; Score 228.5; DB 1; Length 515;
Best Local Similarity 26.2%; Pred. No. 4e-09;
Matches 112; Conservative 59; Mismatches 153; Indels 103; Gaps 26;

QY 43 GGTWLVKQVCKHEDS-----SLQW---SNPAQOTLYFGEKRALDRNRKQLVSTPHEL-- 93
Db 44 GTDVLHCFANPLPSVKITQVTVWQASNGSKQNM-----ALYNTMGVSVLPPEKRV 97
QY 94 -----SISINVALADEGEYTCISPTMPVTKSLVTVGLIPQKPI--ITGYKSS 141
Db 98 EFLRPSFIDGTRLGLELEDEGMYICEFATFPTGNRESQLN-LTWMAKPTNWIETRAV 156
QY 142 LREK---DPAFL--NCOSGSKPAARLTWRKQDELHGEPTROE--DPNGKFTVSSSV 194
Db 157 LRARKGDNKLVTATCTSANGKPPSAVSW---ETRLKGE--AEYQETRNPNNG-TVTVISRY 211
QY 195 TFQVTRDDGASIVCSVNHSLKGAIR-STSQRIEVLVPTAMIRP--DPHPREGQKLIL 252
Db 212 RLVPSEARHQSLACIVNH---LDRFRESLINVQYEPVETIRGFDGNWYLQRTDVKL 267
QY 253 HCEGRNPVQQLWEK-EGSVPLKMTQBSALIP--PFLNKSDSGTYGCTATSNMGSYK 309
Db 268 TKADANPATEYHYHTTLNGLSLPKGVAQNRTLFFRGF-ITYSLAGTYICEATNPIGTRS 326
QY 310 AYTLANVD---PSP-----VPSSSSTYHAIIGGIVAFIVFLLLMILFLGHVLI- 356
Db 327 QQVEVITEFPYTPTEHGRAGQMPT-----ALIGGVAGSV-----LLVLIIVGGIIVA 376
QY 357 ----RH--KGTYLT-----HEAKGSDADPADTATINAEQGQS 388
Db 377 LRRRHTEFGDYSTKHHVGYNGYSKAGIPQHHPMAQNLQVPDSDDEKKA--SPLGSS 434
QY 389 GGDCKE 395
Db 435 YEEEEE 441

RESULT 11
C166_MOUSE STANDARD; PRT; 583 AA.
AC Q61490; Q70136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE (ALCAM) (DM-GRASP protein).
GN ALCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

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RN RP SEQUENCE FROM N.A.
RC STRAIN=NFS;
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajorath J., D'Agid M., Whitney G.S., Palmer D.,
RA Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT conserved in different homologs and mediates cross-species binding.";
RL Eur. J. Immunol. 27:1469-1478(1997).
[2]
RN RP SEQUENCE OF 227-583 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=94376084; PubMed=8089660;
RA Kanki J.P., Chang S., Kuwada J.Y.;
RT "The molecular cloning and characterization of potential chick
RT DM-GRASP homologs in zebrafish and mouse.";
RL J. Neurobiol. 25:831-845(1994).
CC -!- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC THE NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U95030; AAC06342.1; --
CC EMBL; L25274; AAA37528.1; --
CC HSSP; Q13740; 1KJC.
CC MGD; MGI:1313266; Alcam.
CC GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
CC GO; GO:007165; P:signal transduction; IPI.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; IG; 4.
CC SMART; SM00409; IG; 3.
CC PROSITE; PS00835; IG LIKE; 4.
CC PROSITE; PS00290; IG_MHC; FALSE NEG.
CC Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 583 CD166 ANTIGEN.
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 POTENTIAL.
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 120 IG-LIKE V-TYPE 1.
FT DOMAIN 125 234 IG-LIKE V-TYPE 2.
FT DOMAIN 245 328 IG-LIKE C2-TYPE 1.
FT DOMAIN 333 409 IG-LIKE C2-TYPE 2.
FT DOMAIN 416 501 IG-LIKE C2-TYPE 3.
FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 334 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 227 232 PSQKKT -> AAGIPA (IN REF. 2).
```

RT anchored protein (Kilon), a member of the IgLON cell adhesion molecule family". Chem. 274:8224-8230(1999).

RL J. Biol. Chem. 274:8224-8230(1999).

CC -!- FUNCTION: CELL-ADHESION (POTENTIAL).

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -!- TISSUE SPECIFICITY: Highly expressed in brain.

CC -!- PTM: Glycosylated.

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON family.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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DR EMBL: AB017139; BAA75649.1; -.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003598; Ig_c2.

DR Pfam: PF00047; Ig; 3.

DR SMART: SM00408; Igc2; 2.

DR PROSITE: PSS0835; IG_LIKE; 3.

KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;

KW Repeat; Signal.

FT SIGNAL 1 31 KILON PROTEIN.

FT CHAIN 32 ? REMOVED IN MATURE FORM (POTENTIAL).

FT PROPEP 32 348 IG-LIKE C2-TYPE 1.

FT DOMAIN 32 128 IG-LIKE C2-TYPE 2.

FT DOMAIN 133 215 IG-LIKE C2-TYPE 3.

FT DOMAIN 219 307 POTENTIAL.

FT DISULFID 54 112 POTENTIAL.

FT DISULFID 154 197 POTENTIAL.

FT DISULFID 239 291 POTENTIAL.

FT CARBOHYD 67 67 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 280 280 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 348 AA; 37858 MW; 37E90D1C7D24ACAB CRC64;

Query Match 11.2%; Score 233.5; DB 1; Length 348;

Best Local Similarity 24.8%; Pred. No. 1e-09;

Matches 82; Conservative 55; Mismatches 133; Indels 41; Gaps 13;

Qy 9 LLLLLLACWAPGAGNLSDSQPWTSDFTVA--GGTVLKVQVKDHESSLOWNPA 66

Db 15 LAAVLLSLCSCLPAG---QSVDFPMAAVDNMLVRKGDVAVLRCLYLEDGA-SKGAWLNRS 69

Qy 67 QOTLYPGEKALRNRLQVLTSTHESISISNVALADEGETYCSITMPVPTAKSLVTV 126

Db 70 SIIFAGGDKMSV-DPRVSIISLNRKDSLQVQNDVTDGDTYCSVOTQHTPTMQVHLT 128

Qy 127 LGIPKPKIITGYKSLREKDTATLNCSSGSKPAARLTWRKQDGLHGEPTRIQEDPENGK 186

Db 129 VQVPFKIYDINSDTINEGTNVTITCLATG-KPFAISWR-----HISPS-AKPFENGQ 180

Qy 187 TFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSQRIEVLVYTPAM-IRPDPPHPR 245

Db 181 YLDI-----YGITRDQAGEYECSEANDVSFDDVKK--VRVVNFAPTIQIKSGTVTP- 231

Qy 246 EGQKLLHCEGRGNVP-----QVILWEKSGVPPPLKMTQESALLFPFLNKSDSGTYG 298

Db 232 -GRSLRCEGAGVPPPAFEWYKKEKRLFNQGGQGIITNFSTRSILVTWNTQEHFGNYT 290

Qy 299 CTATSNMGYSKAYTYTLNVNDSPPVSSSSTY 329

Db 291 CVAANKLGTWASLPLN-----PPSTAQY 314

RESULT 10

PVRL MOUSE

ID PVRL MOUSE STANDARD; PRT; 515 AA.

AC Q9JUF6; Q9ERL5; Q9JIL7;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).

GN PVRL1 OR PVRL1 OR HVEC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2043787; PubMed=10781093;

RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.;

RT "The murine homolog of human nectin1 delta serves as a species non-specific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20541977; PubMed=11090177;

RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;

RT "Striking similarity of murine nectin-1alpha to human nectin-1alpha (HvEC) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";

RL J. Virol. 74:11773-11781(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Swiss Webster;

RA Zhan J., Wimmer E.;

RT "Mouse nectin-1 (mPR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.

CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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DR EMBL: AF239762; AAF60333.1; -.

DR EMBL: AF270977; AAF76195.1; -.

DR EMBL: AF297665; AAG22808.1; -.

DR MGD; MGI:1926483; Pvr11.

DR GO: GO:0005913; C:cell-cell adhesion junction; IDA.

DR GO: GO:0005515; F:protein binding; IPI.

DR GO: GO:0004872; F:receptor activity; IDA.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003599; Ig.

DR Pfam: PF00047; Ig; 2.

DR SMART: SM00409; Ig; 2.

DR PROSITE: PSS0835; IG_LIKE; 2.

KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;

KW Repeat; Glycoprotein; Signal.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.

FT DOMAIN 31 354 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 355 375 POTENTIAL.

QY 197 QVTREDDGASIVGVNHESLKGADR-STSQRIEVLXTPTAMIRP-DPPHPREQKLLHLC 254
 Db 214 VPSREAHQSLACIVNH---MDRPFESITLVQVEPEVTIEGFGNWMYLRMDVKLTC 269
 QY 255 EGRGNVPQOYLMEK-EGSVPPKMTQESALIPFF-LNKSDSTGYCTATSNMGSKAYY 312
 Db 270 KADANPPATEYHTTLLGSLPKGVEAQNRITLFFKGPINYSLAGTYICEATNPITGRSGQV 329
 QY 313 TLAVND---PS-----PVPSSSTVHALIGGIVAFIVFLLIMLFLGHYLI--- 356
 Db 330 EVNITEFPYTPSPPEHRRAGPVT-----ALIGGVAGSI-----LLVLIVGGIVVALR 379
 QY 357 --RH--KGYLT-----HEAKGSDPADPADTATINAEQSGSG 390
 Db 380 RRHTFKGDYSTKHYVNGYKAGIPQHPPMAQNLQYDPDSDDEKKA--GPLGGSSYE 437
 QY 391 DDKE 395
 Db 438 EEEEE 442

RESULT 8

OPCM_CHICK STANDARD; PRT; 337 AA.
 ID OPCM_CHICK AC Q98892;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Opioid binding protein/cell adhesion molecule homolog precursor
 DE (Neurite inhibitor GP55-A) (OBCAM protein gamma isoform).
 GN OPCML.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
 RT "Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from
 RL chick: structural diversity of IGLON family proteins.";
 RP Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=97157768; PubMed=9004047;
 RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
 RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
 RT are members of the Ig superfamily and are related to OBCAM,
 RT neurotrophin, LAMP and CEPU-1.";
 RL J. Cell Sci. 109:3129-3138(1996).
 CC -1- FUNCTION: Inhibits neurite outgrowth.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
 CC -1- DEVELOPMENTAL STAGE: Increases during development from very low
 CC levels at embryonic day 10 and is most abundant after hatching.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
 CC family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).

DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS00835; IG-LIKE; 3.
 KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Lipoprotein;
 KW Membrane; GPI-anchor; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 314
 FT
 FT PROPEP 315 337
 FT DOMAIN 32 119
 FT DOMAIN 129 211
 FT DOMAIN 215 302
 FT DISULFID 50 108
 FT DISULFID 150 194
 FT DISULFID 236 288
 FT LIPID 314 314
 FT
 FT CARBOHYD 133 133
 FT CARBOHYD 277 277
 FT CARBOHYD 285 285
 FT CARBOHYD 298 298
 SQ SEQUENCE 337 AA; 36887 MW; BAE717551856651E CRC64;
 Query Match 11.3%; Score 235.5; DB 1; Length 337;
 Best Local Similarity 25.3%; Pred. No. 7.2e-10;
 Matches 92; Conservative 58; Mismatches 151; Indels 63; Gaps 16;
 QY 18 CW-----APGGANLSQDDSOPTSDSDE-TVVAGGTVLKCOVKHEDSSLOWSNP 65
 Db 6 CWIVFTATTALLFIPGVPRSGDATPFKAMDNTVTRQGESATLRCVTDVDRV-RRVAILN- 63
 QY 66 AQTLYFGEKRALDRNRIQLVTSHPHELSISINVALADEGYTCISFTMPVPTAKSLVT 125
 Db 64 RSTLYAGNDKWSIDNRVILSKTKQYSIKIHNVVDYDEGPTCSVQTDNHPKTSRVLH 123
 QY 126 VLGIPOKPIITGYKSLREKDTATINCQSSGSKFAARLTWRKGDQLHGEPTRIQEDPNG 185
 Db 124 IVQVFPQIVNISSDITVNEGSSVTLMLCLAFG-RPEPTVTWR-----HLSGK- 169
 QY 166 KTFVTSSSVTFQ---VTREDDGASIVGVNHESLKGADRSTSQRIEVLXTPTAMIRPDP 242
 Db 170 QGF-VSEDEVLITGTITREOSGEYCSANVDVAVDPVRK---VKVTVNY-----PP 216
 QY 243 H-----PREQKLLHCHCEGRGNVPQOYLMEK-----GSVPLPKMTQE---SALIF 286
 Db 217 YISNAXNTGASVGQKILQCEASAVPV-AEFQWFKEDTRLANGLEGVRIESKGRSLTLTF 275
 QY 287 PFLNKDSGTGYCTATSNMGSKAYYTLNVNDRSPVSSSTVHALIGGIVAFIVFLLI 346
 Db 276 FNVSEKDYGNVTCVATNKGNTNA--SIILYGPVAVHDSGNASRAAAGLCIWLTLRL 333
 QY 347 MLIF 350
 Db 334 LLDF 337
 RESULT 9
 KILO RAT
 ID KILO RAT STANDARD; PRT; 348 AA.
 AC Q920J8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kilon protein precursor (Kindred of IGLON).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-62.
 RX MEDLINE=99175207; PubMed=10075727;
 RA Funatsu N., Miyata S., Kumanogoh H., Shigeta M., Hamada K., Endo Y.,
 RA Sokawa Y., Maekawa S.;
 RT "Characterization of a novel rat brain glycosylphosphatidylinositol-

RA Butterfield Y.S.N., Krzyzinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP FUNCTION, AND INTERACTIONS WITH FYB; SCAP2 AND PTK2B.
RX MEDLINE=99401000; PubMed=10469599;
RA Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
RA Schraven B., Neel B.G.;
RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
RT multi-protein complexes in macrophages.",
RL Curr. Biol. 9:927-930(1999).
RN
RP PHOSPHORYLATION BY JAK2, AND INTERACTIONS WITH PTPN11 AND JAK2.
RX MEDLINE=20428742; PubMed=10842184;
RA Stofega M.R., Argentsinger L.S., Wang H., Ullrich A., Carter-Su C.;
RT "Negative regulation of growth hormone receptor/JAK2 signaling by
RT signal regulatory protein alpha.",
RL J. Biol. Chem. 275:28222-28229(2000).
RN [9]
RP FUNCTION, AND INTERACTION WITH CD47.
RX MEDLINE=21400825; PubMed=11509594;
RA Latour S., Tanaka H., Demeure C., Mateo V., Rubio M., Brown E.J.,
RA Maliszewski C., Lindberg F.P., Oldenborg A., Ullrich A.,
RA Deleese G., Sarfati M.;
RT "Bidirectional negative regulation of human T and dendritic cells by
RT CD47 and its cognate receptor signal-regulator protein-alpha:
RT down-regulation of IL-12 responsiveness and inhibition of dendritic
RT cell activation.",
RL J. Immunol. 167:2547-2554(2001).
CC -I- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC as docking protein and induces translocation of PTPN6, PTPN11 and
CC other binding partners from the cytosol to the plasma membrane.
CC Supports adhesion of cerebellar neurons, neurite outgrowth and
CC glial cell attachment. May play a key role in intracellular
CC signaling during synaptogenesis and in synaptic function (By
CC similarity). Involved in the negative regulation of receptor
CC tyrosine kinase-coupled cellular responses induced by cell
CC adhesion, growth factors or insulin. Mediates negative regulation
CC of phagocytosis, mast cell activation and dendritic cell
CC activation. CD47 binding prevents maturation of immature dendritic
CC cells and inhibits cytokine production by mature dendritic cells.
CC -I- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
CC Binds FGR (By similarity). Binds JAK2 irrespective of its
CC phosphorylation status and forms a stable complex. Binds SCAP1
CC and/or SCAP2. The resulting complex recruits FYB. Binds PTK2B.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P78324-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P78324-2; Sequence=VSP_007030;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=P78324-3; Sequence=VSP_007029;
CC Note=No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in brain.
CC Detected on myeloid cells, but not T cells. Detected at lower
CC levels in heart, placenta, lung, testis, ovary, colon, liver,
CC small intestine, prostate, spleen, kidney, skeletal muscle and
CC pancreas.
CC -I- PTM: N-glycosylated.
CC -I- PTM: Phosphorylated on tyrosine residues in response to
CC stimulation with EGF, growth hormone, insulin and PDGF.
CC Dephosphorylated by PTPN11.
CC -I- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC [7]
DR EMBL: D86043; BAA12974.1; -
DR EMBL: Y10375; CAAT71403.1; -
DR EMBL: Y11047; CAAT71944.1; ALT_INIT.
DR EMBL: AB023430; BAA87929.1; -
DR EMBL: AC004832; AAF19260.1; -
DR EMBL: AL034562; CAB38874.1; -
DR EMBL: AL049634; CAB46662.1; ALT_SEQ.
DR EMBL: AL117335; CAC12723.1; -
DR EMBL: BC026692; AAH26692.1; -
DR EMBL: BC03092; AAH3092.1; -
DR EMBL: BC038510; AAH38510.1; -
DR PIR: JCS287; JCS287.
DR Genew: HGNC:9662; PTPNS1.
DR MIM: 602461; -
DR GO: GO:0005886; C:plasma membrane; TAS.
Query Match 11.6%; Score 241.5; DB 1; Length 503;
Best Local Similarity 25.2%; Pred. No. 4.5e-10;
Matches 106; Conservative 64; Mismatches 163; Indels 87; Gaps 20;
QY 8 LLLLLLFAACWAPGAGANLSQDDSPWTSDETVVAGTGVKQVKQKHEDSSI-----Q 61
Db L L L L L L A A C A W A G E E L Q I Q P - D K S V S V A G E S A I L H C T V -----T S L I P V G P I Q 67
QY 62 W ---SNPAQTLVFGFKRALDRNRIQLVTSSTPHE---LSISISNVALADEGEYTCISF-- 113
Db W R G A G P A R E L I Y - N Q E G H F P R V T T S E S T K R E N M D F S I S N I T P A D A G T Y C V K P K 126
QY 114 ----TNPVTA KSLVTLGIPKPIITGYKSLREKDTATLNCQSSGSKPA-ARLTWRKG 168
Db G S P D T E F K S G A G T E L S V R A K P A P V V G P A A R A T P Q H T S F T C E S H G F S P R D I T L K W F K N 186
QY 169 DQELHGEPTRIQEDPNKG--TFTVSSSVTFQVTRDDGASIVCSNVHESI.KGAD-RSTSQ 225
Db G N E L S D F Q N V --D P V G S V S V I H S T A K V I T R E D V H S Q V I C E V A R H T L Q G D P L R G T A N 244
QY 226 RIEVLVPTAMIRPDPPHPRQGLLHHCGRG-NPVPQOYLWEKSGSVPLKMTQESAL 284
Db L S E T I R V P T L E V T Q C P V R A E N Q - V N V T C Q V R K F Y P Q R L Q L T W L E N G V ---S R T E T A S T 300
QY 285 I P P F I N K S D S G T G C T A T S N M G S Y K A Y Y T I N V -----N D P S P V P S ----- 324
Db V ----T E N K D G T Y -----N M S W L L V N V S A H R D D V K L T C Q V E H D G Q P A V S K S H D L K 347
QY 325 -----S S S T V H A I G G -----I V A F T V F L L I L M L F L G H Y L R H K G T Y L T H E A K G S 370
Db V S A H P K E Q G S N T A E N T G S N E R N I Y V V G V C T L L V A L L M A L Y L V R I R -----Q K A Q G S 403
RESULT 7
PVRL HUMAN STANDARD; PRT; 517 AA.
AC Q15223; O75465; Q9HB6; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD111 antigen).
GN PVRL1 OR PRL1 OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;

FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 SQ SEQUENCE 338 AA; 37394 MW; 8FAA60AD98426B4 CRC64;

Query Match 11.7%; Score 245; DB 1; Length 338;
 Best Local Similarity 27.6%; Pred. No. 1.5e-10;
 Matches 86; Conservative 44; Mismatches 152; Indels 30; Gaps 13;

QY 4 PAASLLLLLLPACWAGCANLSDQSPWSTDETVAGGTVVLKCKVKHEDSGLWS 63
 Db 7 PRKQQLPVLLRLCLLPTGLPVRVDFRTGDTNITVROGDTALLCFVED-RSSKVM 65

QY 64 NPAQQLTYFGEKRALDNRIQLVTSTPHLSISISNVALADGEYTCSTFTWPTAKSL 123
 Db 66 N-RSGIIFAGEDKWSLDPRVLEKRPLEYSRLRIQKVDVDEGYSYTCVQTOHPKTSQV 124

QY 124 VTVLGTPQPIITGYKSSLRKDTATINCOSSGSKPAARLTWRKGGQELHGPETRIQEDP 183
 Db 125 YLIVQPPKLSNDSITWEGNSVTLVCMANG-RPEPVITWR-----HLPT----- 171

QY 184 NGKTFVTSSSV--TFQVTRDDGASIVCSVNHBSLKGADRTSQRIEVLVYPTTAMIRPDP 241
 Db 172 -GKEFGESEYELILGITREQSG-KYEKAANE-VASAD-VKQVRVTNVYPT-ITESKS 226

QY 242 PHPRGQKLLHCEGRGNVPQOYLWEKE-----GSVPPLQMT-QESALFFFLNKSUS 294
 Db 227 NEAATGRQALLRCEASAVPTP-DFEYWRDTRINSANGLEIKSTGSQLVMANVTTEHY 285

QY 295 GTYGCTATSNMG 306
 Db 286 GNTCVANAKLG 297

RESULT 6

SHS1_HUMAN STANDARD; PRT; 503 AA.
 AC P78324; O00683; O43799; Q8N517; Q8TAL8; Q9H022; Q9UDX2; Q9UIJ6;
 AC Q9Y4U9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
 DE (SHP substrate-1) (SHP-1) (Inhibitory receptor SHPS-1) (Signal-
 DE regulatory protein alpha-1) (SHP-alpha-1) (SHP-alpha-2) (SHP-alpha-
 DE 3) (MYD-1 antigen) (Brain Ig-like molecule with tyrosine-based
 DE activation motifs) (Bit) (Macrophage fusion receptor) (p84).
 GN PTPNS1 OR SHPS1 OR SHP OR MYD1 OR BIT OR MFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=97223399; PubMed=9070220;
 RA Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,
 RA Fujioaka Y., Kasuga M.;
 RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
 RT localization of genes.";
 RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1), POLYMORPHISM, PHOSPHORYLATION,
 RP N-GLYCOSYLATION, AND INTERACTIONS WITH PTPN11, PTPN6 AND GRB2.
 RC TISSUE=Placenta;
 RX MEDLINE=97215901; PubMed=9062191;
 RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
 RA Ullrich A.;
 RT "A family of proteins that inhibit signalling through tyrosine kinase

RT receptors.";
 RL Nature 386:181-186(1997).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANTS ASP-95; LEU-96; ASN-100;
 RP ARG-107; GLY-109 AND VAL-131.
 RP TISSUE=Monocytes;
 RX MEDLINE=98143722; PubMed=9485180;
 RA Brooke G.P., Parsons K.R., Howard C.J.;
 RT "Cloning of two members of the SHP alpha family of protein tyrosine
 RT phosphatase binding proteins in cattle that are expressed on monocytes
 RT and a subpopulation of dendritic cells and which mediate binding to
 RT CD4 T cells.";
 RL Eur. J. Immunol. 28:1-11(1998).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-44; THR-50; THR-52;
 RP ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107; GLY-109 AND
 RP VAL-131.
 RC TISSUE=Brain;
 RX MEDLINE=20053880; PubMed=10585853;
 RA Sano S.-I., Ohnishi H., Kubota M.;
 RT "Gene structure of mouse BIT/SHPS-1.";
 RL Biochem. J. 344:667-675(1999).
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Gardner C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Coulson A., Coville G.J., Deadman R., Connor R.E., Corby N.R.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekoske K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharasliho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [6]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; THR-50;
 RP THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107;
 RP GLY-109 AND VAL-131.
 RC TISSUE=Brain, Kidney, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltan E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,


```
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AF308632; AAG30281.1; -
CC HSSP; P06907; INEU.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 2.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
FT Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
FT CARBOHYD 332 332
SQ SEQUENCE 515 AA; 57047 MW; 5FAB00320DD3785 CRC64;
Query Match 12.0%; Score 250.5; DB 1; Length 515;
Best Local Similarity 26.9%; Pred. No. 1e-10;
Matches 116; Conservative 54; Mismatches 157; Indels 105; Gaps 25;
Qy 43 GGTVTLCQVKD-----EDSLWS-----NPAQOTLYGEXRALDRNIQL 85
Db 44 GTDVLHCSFANPLGPKITQVTWQKATNGSKONVATNPANGSVLAPYR-----ERVEF 99
Qy 86 VTSTPHSLISISNVALADEGYTCSTPTMPRTAKSLVTLVLPQKPI--ITGYKSLR 143
Db 100 LRPSFTDGTIRLSLELEDEGVYICEFATPAGNRESQLN-LTWAKPTNWIEGTQAVLR 158
Qy 144 E---KDTATL--NCQSSGSKPAARLTWRKQDQLHGEPTRIQE--DNGKFTVSSVTF 196
Db 159 AKGKDDKVLVATCTSANGKPPSVVSW---ETHLKGE-AEYQETRNPNP-TVTVISRYRL 213
Qy 197 QVTREDDGASTVCSVNHESLKGADR-SPSQRIEVLTYPTAMIRP-DPHPRREGQKLLHC 254
Db 214 VPSREDHRQSACLVNH-----MDFRESLTNVQYEPEVTIEGFDGNWYLQRMVKKLC 269
Qy 255 EGRGNPVPQQYLWEK-EGSVPLKMTQBSALIF--PFLNKSDSGTYGCTATSNMGYSKAY 311
Db 270 KADANPPATEYHTWTLNLSLPGVEAQNRTLFFRGP-INYSMAGTYICEATNPITRSQG 328
Qy 312 YTLNVD-----PSP-----VPSSSSTVHAIGGIVATVIFLLIMLIFLGHYLL-- 356
Db 329 VEVNITEFTFPSPPEHGRAGQVPT-----AIGGVVGS-----LVLVFWVGIVVAL 378
Qy 357 ---RH--KGTYLTHE-----AKGSD-----APDADTALIN 382
Db 379 CRRRTFTKGDYTKKHVYNGVSKAGIQPHPPMAQNLOYPEDSDDEKXAGPLGSSVEE 438
Qy 383 AEGQSGGDDKK 394
Db 439 EEEBEGGGGERK 450
RESULT 4
PVR2_MOUSE
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ID AC P32507; Q62096; STANDARD; PRT; 530 AA.
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
GN PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene.";
RL J. Virol. 66:2807-2813 (1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus.";
RL J. Biol. Chem. 269:8431-8438 (1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.R., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey C., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.B., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)
RT mediates entry of pseudorabies virus but not herpes simplex virus
RT types 1 and 2.";
RL J. Virol. 73:4493-4497 (1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHHERPESVIRUS (SUCH AS MURINE HSV) ENTRY
CC INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta; isoId=P32507-1; Sequence=Displayed;
CC Name=Alpha; isoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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DR EMBL; M24407; AAA36461.1; -
 DR EMBL; M24406; AAA36462.1; -
 DR EMBL; X64116; CAA45478.1; -
 DR EMBL; X64117; CAA45478.1; JOINED.
 DR EMBL; X64118; CAA45478.1; JOINED.
 DR EMBL; X64119; CAA45478.1; JOINED.
 DR EMBL; X64120; CAA45478.1; JOINED.
 DR EMBL; X64121; CAA45478.1; JOINED.
 DR EMBL; X64122; CAA45478.1; JOINED.
 DR EMBL; X64123; CAA45478.1; JOINED.
 DR EMBL; X64117; CAA45479.1; JOINED.
 DR EMBL; X64118; CAA45479.1; JOINED.
 DR EMBL; X64119; CAA45479.1; JOINED.
 DR EMBL; X64120; CAA45479.1; JOINED.
 DR EMBL; X64121; CAA45479.1; JOINED.
 DR EMBL; X64122; CAA45479.1; JOINED.
 DR EMBL; X64123; CAA45479.1; JOINED.
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 DR EMBL; X64118; CAA45480.1; JOINED.
 DR EMBL; X64119; CAA45480.1; JOINED.
 DR EMBL; X64120; CAA45480.1; JOINED.
 DR EMBL; X64121; CAA45480.1; JOINED.
 DR EMBL; X64122; CAA45480.1; JOINED.
 DR EMBL; X64123; CAA45480.1; JOINED.
 DR EMBL; AC068948; AAF69803.1; -
 DR PIR; A43024; RWHUPD.
 DR PIR; S12048; RWHUPA.
 DR Genew; HGNC:19705; PVR.
 DR MIM; 173850; -
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007125; F:invasive growth; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 3.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; Antigen; Alternative splicing; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 417
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 328
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 105 105
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 218 218
 FT CARBOHYD 237 237
 FT CARBOHYD 278 278
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT CARBSPLIC 340 384
 FT VARSPLIC 331 331
 FT VARSPLIC 332 384
 FT VARSPLIC 385 392
 FT VARSPLIC 393 417
 FT VARSPLIC 67 67
 FT VARIANT 67 67
 FT FTID=VAR_003952.

FT VARIANT 340 340 I -> M (in dbSNP:203710).
 FT FTID=VAR_011736.
 SQ SEQUENCE 417 AA; 45302 MW; D15C012CB853169B CRC64;
 Query Match 13.4%; Score 280; DB 1; Length 417;
 Best Local Similarity 28.0%; Pred. No. 6e-13;
 Matches 108; Conservative 50; Mismatches 158; Indels 70; Gaps 17;
 QY 5 AASLLLLLLFACWAPGGANLSQDSQPWTSDETVVA-----GGTVVLKC--QVKD 54
 DB 7 AAWPLLVLALLVLSWPP-----PGTGDVVVQAPTQVPGFLGDSVILPCYLQVFN 55
 QY 55 HE---DSSLQSNPAQOTLYFGEKAL-----RDNRIQLVSTSTPHELSISIN 99
 DB 55 MEVTHVSQLTWAR-----HGESGMAVFHOTQGPSYSESKLEFVAA---RLGAELRN 105
 QY 100 VAL-----ADEGYTCSIFMPRTAKSLVTVLIGIPQKPIITG--YKSSIREKDTATL 150
 DB 105 ASLRMFGLRVEDENYTCFLVTFPP--QGSRSVDIWLRLAKPONTAEVQVKQLTGEPVMA 164
 QY 151 NCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPN--GKTFTVSSSVTFQVTRDDGASIV 208
 DB 165 RCVSTGGRPPAQITWH---SDLGMPNTSQV--PGFLSGTIVTSLMILVPPSQVDGKNVT 220
 QY 209 CSVNHESLKGAADRSTSORIEVLYTPTAMIRPPDPPHREGQ-KLLHCEGRGNVPQQYLW 267
 DB 221 CKVEHESPEKPOLLT-VNLTVVYPPEVSISGYDNNWYLCQNEATLTCDARSNPEPTGYNW 279
 QY 268 EKE-GSVPLKMTQESALIPFLNKSQDSCTYCTATSNMGSYKAYITLNNPSPVSSS 326
 DB 280 STTMGLPPFAVAQAQLIRVDPNPITLTCNVTNALGARQALTVQVKSGPFPSEHSG 339
 QY 327 STYHALIGGIVAFIVFLMLIMLIFLG 352
 DB 340 ISRNAIL-----FLVLGILVFLILLG 360
 RESULT 3
 ID_PVR1_PIG STANDARD; PRT; 515 AA.
 AC Q9GL76;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).
 GN PVR1L OR PVR1 OR HVEC.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21176378; PubMed=11277703;
 RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;
 RT "Porcine HvEC,
 RT is a functional alphaherpesvirus receptor.";
 RT Virology 281:315-328(2001).
 CC -/- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPEVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -/- SUBUNIT: Interacts with HSV glycoprotein D (gp) (By similarity).
 CC -/- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -/- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -/- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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DR PROSITE; P50835; IG-LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 85 85
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 237 237
FT CARBOHYD 278 278
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FT CARBOHYD 313 313
FT VARSPLIC 386 392
FT VARSPLIC 393 417
FT SEQUENCE 417 AA; 45464 MW; DA4AD0F6AD2F6E1F CRC64;
Query Match 13.7%; Score 285.5; DB 1; Length 417;
Best Local Similarity 26.2%; Pred. No. 2.4e-13;
Matches 112; Conservative 56; Mismatches 189; Indels 71; Gaps 17;
QY 10 LLLLLFACCPAGCANLSQDDSQSQTWSTETVA-----GGTVVLKC--QVKDHD-- 57
DB 12 LLLTLLLSWPP-----PQTGDIIVQATQVPGFGDSVTLPVLOVPCMEETH 60
QY 58 -SSIQWNPQAQ-----QTLFGKRALRDNRIQLVLTSTPHELSISINVALADEG 106
DB 61 VSQLTWSEHGSGSMVAFHQOGPNYSEPKLEFVAARLGTTEL-RDASLRMFLGRVEDEG 119
QY 107 BYTCSIFMPVTRAKSLVTLGIGIQKPIITG--YKSSIREKDTATLNCQSGSPARALT 164
DB 120 NYTCLFTVTFP-QGSRSDVIMLRVLAKPQNTAEVQVLTGKFPVVARCVSTGGPPPAHIT 178
QY 165 WRKGDQELHGEPTRIOEDPN--GKTFVSSSVTFQVREDGASIVCSWNHSLKGDARS 222
DB 179 WH---SDUGGNPNSQA-PGFLSGTIVTWSLWILPSSQVDGKSVTKVEHSEKXPQLL 234
QY 223 TSQRIEVLVTTAMIRP-DPPHPREGQKLLHLHCEGRGNPVPQQYLWEKE-GSVPLPKMTQ 280
DB 235 T-VNLTVYPPPEVSIISGYDNNWYLSQNEATLTCDAKSNPEPTGYNWSVTMGLPFPFAVQ 293
QY 281 ESALIFPFLKSDSTGYCTATSNMGSVYKAYTLNVND-PSPVPSSTYHAIIGGIIVAF 339
DB 294 CAQLLRFPVDFKINTFTICNVNALGQAELTVQKSGPPSPSGMSS-----NLIIF 347
QY 340 IVFLLLMILFLG-----HYLIRHKGTYLTHEAKGSDDAPDADTAIIN 382
DB 348 LILGLVILLTLLGIGVYFRSCRSREFLWCHLSFSSSEHASASANGYISYSDVGREASS 407
QY 383 ABGQSGG 390
DB 408 SQDPQTEG 415
RESULT 2
PVR HUMAN
ID PVR HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
sequence, and expression of a new member of the immunoglobulin
superfamily.";
RL Cell 56:855-865(1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RT Takeuchi K., Takegami T., Nomoto A.;
RL "The poliovirus receptor protein is produced both as membrane-bound
and secreted forms.";
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyanni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RT Shamor M., Brower A., Olsen A.S., Smith L.M.;
RL "Sequence analysis of a 1mb region in 19ql3.2 containing a zinc finger
gene cluster.";
RN [5]
RP Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
gamma). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Name=Alpha;
IsoId=P15151-1; Sequence=Displayed;
Name=Beta;
IsoId=P15151-2; Sequence=VSP_002617;
Name=Gamma;
IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
Name=Delta;
IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
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```

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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 8.4531 seconds

(without alignments)
2451.636 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPASLLLLLLLFFACWA.....AIIAEGGSGGDDKKEYFI 398

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	285.5	13.7	417	1	PVR CERAE
2	280	13.4	417	1	PVR CERAE
3	250.5	12.0	515	1	PVR1 PIG
4	250	12.0	530	1	PVR2 MOUSE
5	245	11.7	338	1	LAMP CHICK
6	241.5	11.6	503	1	SHS1 HUMAN
7	239	11.5	517	1	PVR1 HUMAN
8	235.5	11.3	337	1	OPCM CHICK
9	233.5	11.2	348	1	KILO RAT
10	228.5	11.0	515	1	PVR1 MOUSE
11	228.5	11.0	583	1	C166 MOUSE
12	228	10.9	538	1	PVR2 HUMAN
13	226.5	10.9	506	1	SHS1 BOVIN
14	225.5	10.8	338	1	LAMP RAT
15	225.5	10.8	583	1	C166 HUMAN
16	225	10.8	338	1	LAMP HUMAN
17	224	10.7	513	1	SHS1 MOUSE
18	221.5	10.6	702	1	CEA5 HUMAN
19	218.5	10.5	739	1	VCA1 RAT
20	217	10.4	509	1	SHS1 RAT
21	216	10.4	345	1	OPCM RAT
22	215	10.3	345	1	OPCM HUMAN
23	213	10.2	344	1	PVR1 HUMAN
24	212	10.2	4391	1	PGSM HUMAN
25	211	10.1	345	1	OPCM BOVIN
26	205	9.8	344	1	NTRI MOUSE
27	204	9.8	344	1	NTRI RAT
28	202.5	9.7	353	1	CEPU CHICK
29	197.5	9.5	588	1	C166 CHICK
30	194.5	9.3	403	1	RAGE MOUSE
31	194.5	9.3	3707	1	ICB3 HUMAN
32	194	9.3	547	1	ICB3 HUMAN
33	191.5	9.2	555	1	C166 CARAU

34	191	9.2	764	1	ICCR DROME
35	190.5	9.1	646	1	MU18 HUMAN
36	189.5	9.1	1447	1	DCC MOUSE
37	188	9.0	628	1	LJ HUMAN
38	187	9.0	387	1	SRB2 HUMAN
39	186	8.9	1241	1	NPHN HUMAN
40	181.5	8.7	564	1	C166 BRARE
41	181.5	8.7	1443	1	NEO1 CHICK
42	181	8.7	1377	1	NEO1 RAT
43	179	8.6	344	1	CEA6 HUMAN
44	178.5	8.6	398	1	SRB1 HUMAN
45	178.5	8.6	3375	1	UN52_CABEL

ALIGNMENTS

RESULT 1
PVR CERAE
ID PVR CERAE STANDARD; PRT; 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=3059651; PubMed=1331508;
RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain";
RL J. Virol. 66:7059-7066(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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or send an email to license@isb-sib.ch).

CC EMBL; D12611; BAA02136.1; -;
CC EMBL; D12612; BAA02137.1; -;
CC PIR; A44194; A44194.
CC PIR; B44194; B44194.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; IG; 3. 1.
CC SMART; SM00406; IGV; 1.

Q08180	drosophila
P43121	homo sapien
P70211	mus musculus
P50895	homo sapien
Q9plw8	homo sapien
O60500	homo sapien
Q90460	brachydanio
Q90610	gallus gall
P97603	rattus norv
P40199	homo sapien
O00241	homo sapien
Q06561	caenorhabdi

Search completed: May 27, 2004, 09:32:27
Job time : 12.5056 secs

Db 100 LPSPTDGTIRLSRLEDEGVYICFATFTGNRESQLN-LTVMAKPTNWIETGQAVLR 158
QY 144 EK---DTATL--NCQSSGSKPAARLWTKGDQELHGEPTRIQEDPNG--KTFVSSVTFP 196
Db 159 AKKGQDKVLVATCATSANGKPPSVWSW---ETRLKGE-ARVFGDSGTMAPVTVISRYRL 214
QY 197 QVTREDDGASIVCSVNHESLKGADR-STSQREVLVLTPTAMIRP-DPPHPRGGQKLLHLC 254
Db 215 VPSREAHQSLACIVNYH-----MDRPEKSLTLNVQEPVETIEGDFGNWYLRQMDVKLTC 270
QY 255 EGRGNVPVPOQLWEK-EGSVPLPKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAY 312
Db 271 KADANPPATEYHWTTLGSLPKGVEAQNLTFFKGPINYSLAGTYICEATNPIGTRSGQV 330
QY 313 TLNVND-----PS-----PVPSSSYTHAIIIGVAFIVFELLMLLFIHGYLI--- 356
Db 331 EVNITEFPYTPSPPEHRRAGVPPT-----AIIIGVAGSI-----LLVLIVVGGIVVALR 380
QY 357 --RH--KGYLT-----HEAKSGDDADPADTATINAEQSGSG 390
Db 381 RRRHTPKGYISTKHVYNGYSGKAGIPQHHPPMAQNLQVPDDSDDEKKA--GPLGSSSYE 438
QY 391 DDKKE 395
Db 439 EEEEE 443

RESULT 15
A36319
N:Alternate names: CEA; meconium antigen 100
C:Species: Homo sapiens (man)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text change 31-Jan-2000
C:Accession: A36319; A27773; A31037; A25845; S08106; S31737; A4476; I54224; I59098; A26831
R:Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Haseauer, M.; Shively, M.
Mol. Cell. Biol. 10, 2738-2748, 1990
A:Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its prom
A:Reference number: A36319; MUID:90258861; PMID:2342461
A:Accession: A36319
A:Molecule type: DNA
A:Residues: 1-702 <SCH>
A:CROSS-references: GB:M17303; NID:g178676; PIDN:AA559513.1; PID:g178677
A:Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-Thr
R:Reauchenin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A:Title: Isolation and characterization of full-length functional cDNA clones for human
A:Reference number: A27773; MUID:88038876; PMID:3670312
A:Accession: A27773
A:Molecule type: mRNA
A:Residues: 1-702 <BEA>
A:CROSS-references: GB:M29540; NID:g180222; PIDN:AA51967.1; PID:g180223
R:Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
A:Reference number: A31037; MUID:89122014; PMID:3220478
A:Accession: A31037
A:Molecule type: mRNA
A:Residues: 1-702 <BAR>
A:CROSS-references: GB:M29540; NID:g180222; PIDN:AA51967.1; PID:g180223
A:Note: the authors translated the codon GTG for residue 130 as Leu
R:Oikawa, S.; Nakazato, H.; Kosaiki, G.
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A:Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
A:Reference number: A25845; MUID:87128144; PMID:3814146
A:Accession: A25845
A:Molecule type: mRNA
A:Residues: 5-702 <OIK>
A:CROSS-references: GB:M15042; NID:g180198; PIDN:AA51963.1; PID:g180199
R:Oikawa, S.
submitted to the EMBL Data Library, September 1989
A:Reference number: S08106
A:Accession: S08106

A:Molecule type: mRNA
A:Residues: 5-319,321-702 <OIT>
A:CROSS-references: EMBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
R:Barnett, T.
submitted to the EMBL Data Library, September 1991
A:Description: Genomic DNA sequence upstream of the translational start of the carcinoem
A:Reference number: S31737
A:Accession: S31737
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <BA2>
A:CROSS-references: EMBL:X62151
R:Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Brenner, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A:Title: Identification of three new genes and estimation of the size of the carcinoemb
A:Reference number: A4476; MUID:93052339; PMID:1427854
A:Accession: A4476
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 35-141 <KHA>
R:Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A:Title: Characterization of the genomic organization of human carcinoembryonic antigen
A:Reference number: I54224; MUID:91139118; PMID:2286372
A:Accession: I54224
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:CROSS-references: GB:M60964; NID:g180215; PIDN:AAA51964.1; PID:g180217
R:Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A:Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon
A:Reference number: I59098; MUID:87204247; PMID:3033671
A:Accession: I59098
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 331-702 <RE2>
A:CROSS-references: GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:g180241
R:Siepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
Biochem. Biophys. Res. Commun. 147, 212-218, 1987
A:Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105
A:Reference number: A26831; MUID:87326349; PMID:3632664
A:Accession: A26831
A:Molecule type: protein
A:Residues: 35-64 <SIE>
R:Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A:Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at t
A:Reference number: A35490; MUID:90321257; PMID:2372297
A:Accession: A35490
A:Molecule type: protein
A:Residues: 'X', 140-151, 'X', 153, 'X', 155-156 <THO>
A:Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer
C:Comment: This heavily glycosylated membrane protein of unknown function is a widely use
C:Genetics:
A:Gene: GDB:CEA
A:CROSS-references: GDB:119054; OMIM:114890
A:Map position: 19q13.2-19q13.2
A:Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-678/Product: carcinoembryonic antigen #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:338-395/Domain: immunoglobulin homology <IMM3>
F:516-573/Domain: immunoglobulin homology <IMM4>
F:608-657/Domain: immunoglobulin homology <IMM5>
F:679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC5288
R:Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
A:Reference number: JC5287; MUID:97223399; PMID:9070220
A:Contents: Brain
A:Accession: JC5288
A:Molecule type: mRNA
A:Residues: 1-509 <YAM>
A:CROSS-references: DDBJ:D87967; NID:g1864012; PIDN:BAAL3520.1; PID:g1864013
C:Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C:Genetics:
A:Gene: shps-1
A:Map position: 2

Query Match 10.7%; Score 224; DB 2; Length 509;
Best Local Similarity 26.5%; Pred. No. 9.4e-09;
Matches 112; Conservative 51; Mismatches 170; Indels 90; Gaps 20;

QY 8 LLLLLLFFACCCWAPGGANLQDDSQPWTSDFTVAGTIVLKCQVXDHDSSSLQWSNPAQ 67
DB 14 LLLLLLLSACFCGTGKELKVTPQPKS-VSVAAGDSTVLNCTL-----TSLLPVGPPIK 67

QY 68 QTLFFGEKRAL-----RDNRILQVTSPTH-ELSSISINVALADEGEYTCISIF--- 113
DB 68 WYRGVQGSRLLIYFTGEHFPRTVNSDATKRNNDFFSIRISNVTPEADAGTYICVKFQKG 127

QY 114 -TMPVRTAKS-----LVTVLGIPIQKPIITGYKSSLRKEDTATLNCQSSGSKPA-ARLTWRK 167
DB 128 PSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTCKSHGFSRNTILKWFK 187

QY 168 GQQLHGEPTRIQEDPNCK--TFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSQ 225
DB 188 DQQLHLETTV--NPSGKNVSYNISSTVRVLSMDVHVKVCEVAHITL---DRSPLR 242

QY 226 RIE-----VLYTPTAMIRPDPPHREGOKLLHCEGRNPVPQOYLWEKGSV-----PPL 276
DB 243 GIANLSNFIKVSPTVKVQTSPTSMNQVNLTCRAE-RFYPEDLQLIWLNGVSRNDTPK 301

QY 277 KMTQESALIFPFLNKSDSGTYGCTA-----TSNMGSKAYTYTLNV-NDPSV----- 322
DB 302 NLT-----KNTDGTNYTSLFLVNSAHRDVFVTCQVXHDQOOPAITRNHTVLG 350

QY 323 -----PSSSST--YHAIIGGVAFIVFLLIMLIFLGHYLIRHKGYLTHTHEA 367
DB 351 LAHSSDQSGMQTFPGNATHNNVFIQVGVV---CALLVLLMAALYLIRIK-----QKKA 403

QY 368 KGS 370
DB 404 KGS 406

RESULT 13
JC5289
SHP substrate-1 protein, 513 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC5289
R:Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
A:Reference number: JC5287; MUID:97223399; PMID:9070220
A:Contents: Brain
A:Accession: JC5289
A:Molecule type: mRNA
A:Residues: 1-513 <YAM>
A:CROSS-references: DDBJ:D87968; NID:g1864014; PIDN:BAAL3521.1; PID:g1864015
C:Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C:Genetics:
A:Gene: shps-1

A:Map position: 2

Query Match 10.7%; Score 224; DB 2; Length 513;
Best Local Similarity 26.5%; Pred. No. 9.5e-09;
Matches 112; Conservative 51; Mismatches 170; Indels 90; Gaps 20;

QY 8 LLLLLLFFACCCWAPGGANLQDDSQPWTSDFTVAGTIVLKCQVXDHDSSSLQWSNPAQ 67
DB 14 LLLLLLLSACFCGTGKELKVTPQPKS-VSVAAGDSTVLNCTL-----TSLLPVGPPIK 67

QY 68 QTLFFGEKRAL-----RDNRILQVTSPTH-ELSSISINVALADEGEYTCISIF--- 113
DB 68 WYRGVQGSRLLIYFTGEHFPRTVNSDATKRNNDFFSIRISNVTPEADAGTYICVKFQKG 127

QY 114 -TMPVRTAKS-----LVTVLGIPIQKPIITGYKSSLRKEDTATLNCQSSGSKPA-ARLTWRK 167
DB 128 PSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTCKSHGFSRNTILKWFK 187

QY 168 GQQLHGEPTRIQEDPNCK--TFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSQ 225
DB 188 DQQLHLETTV--NPSGKNVSYNISSTVRVLSMDVHVKVCEVAHITL---DRSPLR 242

QY 226 RIE-----VLYTPTAMIRPDPPHREGOKLLHCEGRNPVPQOYLWEKGSV-----PPL 276
DB 243 GIANLSNFIKVSPTVKVQTSPTSMNQVNLTCRAE-RFYPEDLQLIWLNGVSRNDTPK 301

QY 277 KMTQESALIFPFLNKSDSGTYGCTA-----TSNMGSKAYTYTLNV-NDPSV----- 322
DB 302 NLT-----KNTDGTNYTSLFLVNSAHRDVFVTCQVXHDQOOPAITRNHTVLG 350

QY 323 -----PSSSST--YHAIIGGVAFIVFLLIMLIFLGHYLIRHKGYLTHTHEA 367
DB 351 LAHSSDQSGMQTFPGNATHNNVFIQVGVV---CALLVLLMAALYLIRIK-----QKKA 403

QY 368 KGS 370
DB 404 KGS 406

RESULT 14
JC4024
poliovirus receptor-related protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C:Accession: JC4024
R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr
Gene 155, 261-265, 1995
A:Title: Complementary DNA characterization and chromosomal localization of a human gene
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
A:Reference number: JC4024; MUID:95237621; PMID:7721102
A:Accession: JC4024
A:Molecule type: mRNA
A:Residues: 1-518 <LOP>
A:CROSS-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C:Genetics:
A:Gene: GDB:PVRR1
A:CROSS-references: GDB:583951
A:Map position: 11q23-11q24
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F:356-379/Domain: transmembrane #status predicted <TMM>
F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.6%; Score 221.5; DB 2; Length 518;
Best Local Similarity 25.9%; Pred. No. 1.5e-08;
Matches 110; Conservative 52; Mismatches 166; Indels 97; Gaps 23;

QY 43 GGTIVLKCQVXDHDSS-----SLQWS-----NPAQQTLYFGEKRALRNRILQ 85
DB 44 GTDVVLHCSFANPLPSVKITQVTQKSTNGSKQNVAINYPNSGVSLAPYR-----ERVEF 99

QY 86 VTSTPHELSSISINVALADEGEYTCISFTMPVRTAKSLVTLVIGIPQKPI--ITGKSSLR 143

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-538 <RES>

A;Cross-references: GB:S79172; NID:g1042204; PID:g1042205

C;Genetics:

A;Gene: PRK2delta

C;Superfamily: poliovirus receptor; immunoglobulin homology

F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 228; DB 2; Length 538;
Best Local Similarity 24.6%; Pred. No. 5.1e-09;
Matches 93; Conservative 53; Mismatches 160; Indels 72; Gaps 15;

QY 8 LLLLLLFFACWAPGGANLSQDDSPWTSDETIVVAGTVVLKQV----- 52
DB 21 LLLLLL-----ETGA---QDVRVQLPEVRGQLGGTVLPCHLLPPVPLVLSLVTWQ 71
QY 53 -----KHED-----SSLWSNPAQOTLYF--GEKALRDNRILQVLTSTPHELIS 96
DB 72 RPDAPANHONVAAPHKXGFPSPKPGSERLSFVSAKSTGQDTEAELQDAT-----LA 126
QY 97 ISNVALADEGEYTCISFTMPVRTAKSLVTVLGIPOKP--IITGVKSLREKDTATLNCOS 154
DB 127 LHGUTVDEGNICEPATFPKGVGRM-TWLRLVIAKPKNAEAKQVTFSDPTVALCIS 185
QY 155 SGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHE 214
DB 186 KEGPPARISW-LSSLWEAKETQVSGTLAG-TVTVTSRFTLVPSGRADGVTVTCCKVEHE 243
QY 215 SLKGADSTSORIEVLTPPAMI-----RPDPHPRREGOKLLHCEGRGNPVPOQ 264
DB 244 SFE-EPALIPVTLVSRYPPVEVSGYDNNVYLGTD-----ATLSCDVRNPSPTG 293
QY 265 YLWE-KEGSPVPLKMTQESALIFPLKNSDGTGCTATSNMGSYKAYITLNVNDPSPVP 323
DB 294 YDSTTSGTPTSAVAGSOLVIAVDSLENTFTVCTVNAVGNVGRABQVIFVE-TPNT 352
QY 324 SSGSYTHAIIIGVAVFIV 341
DB 353 AGAGATGGIIGIIFAAII 370

RESULT 10

I39428

alcam - human

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C;Accession: I39428

R;Bowen, M.A.; Patel, D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marquardt, H.

J. Exp. Med. 181, 2213-2220, 1995

A;Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion mol

A;Reference number: I39428; MUID:95279947; PMID:7760007

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-583 <RES>

A;Cross-references: GB:I38608; NID:g886257; PIDN:AA859499.1; PID:g886258

Query Match

Best Local Similarity 10.8%; Score 225.5; DB 2; Length 583;

Matches 80; Conservative 70; Mismatches 148; Indels 59; Gaps 14;

QY 2 GAPAASLLLLLFFACWAPGGANLSQDDSPWTSDETIVVAGTVVLKQVY----- 53
DB 5 GASSCRLLFCLLISATVFRPG-----LGWTVNSAY-GDTIIIPCRDLVQNLNMF 54

QY 54 -----DHESS---LWSNPAQOTLYFGEKALRDNRILQVLTSTPHELISISNVALADEG 106
DB 55 KMRYEKPDGSPVFTAFRSSTKSVQYDDVPYKO-RLNL-----SENYTLISINARISDEK 109

QY 107 EYTCISFTMP-VRTAKSLVTVLGIPOKPIITGVKSLREKDTATL-NCOSGSKPAARLT 164
DB 110 RFVCMVLTEDNVFEAPTIVKVKQPSKEIVSKALFLETEQKLLGDCISESDSPDGNIT 169

QY 165 WRKGDQELH---GEPTRI---QEDPNKGTFTVSSSVTFQVTRDDGASIVCSVNHESLKG 218
DB 170 WYRNGKVLHLEGAVVILFEKEMDPVTQLYTWTSTLETKTKRADIQMPFTCSVTYTGPSG 229
QY 219 ADR-STSORIEVLVYTPAMIR-----PDPHPREGOKLLHCEGRGNPVPOQYLWREKGSV 273
DB 230 QKTIHSEQAVFDIYPTQVTTQVLPKNAIKEGDNITLKLONGNPPPEEFLLFYLPQQP 289
QY 274 PPLKMTQESALIFPLKNSDGTGCTATSNMGSYKAYITLNVNDPSPVPSSSYTH 330
DB 290 EGRSSNTYTLN--DVRNATGDYKCSL-----IDKKSMTASTAITVH 330

RESULT 11

JC4776

limbic-system-associated membrane protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 19-May-2000

C;Accession: JC4776

R;Pimenta, A.F.; Fischer, I.; Levitt, P.

Gene 170, 189-195, 1996

A;Title: cDNA cloning and structural analysis of the human limbic-system-associated mem

A;Reference number: JC4776; MUID:96235133; PMID:8666243

A;Accession: JC4776

A;Molecule type: mRNA

A;Residues: 1-338 <PIM>

A;Cross-references: GB:U41901; NID:g1276898; PIDN:AA50569.1; PID:g1276899

A;Experimental source: brain

C;Comment: This is a neuronal surface glycoprotein distributed in cortical and subcort

C;Genetics:

A;Gene: lamp

C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

C;Keywords: brain; glycoprotein; membrane protein; phosphoprotein

F;1-7/Domain: signal sequence #status predicted <SIG>

F;333-338/Region: hydrophobic

F;40,66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status prec

F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predicted

F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 10.8%; Score 225; DB 2; Length 338;

Best Local Similarity 25.4%; Pred. No. 4.7e-09;

Matches 91; Conservative 55; Mismatches 172; Indels 40; Gaps 15;

QY 4 PAASLLLLLFFACWAPGGANLSQDDSPWTSDETIVVAGTVVLKQVQKHEDSSIQWS 63
DB 7 PDRKQLPLVLLRLCLLPTGLPVRSVDFNRGTDNITVRQDGTAILRCVLED-KNSKVAVL 65

QY 64 NPAQOTLYFGEKALRDNRILQVLTSTPHELISISNVALADEGEYTCISFTMPVRTAKSL 123
DB 66 N-RSGIIFAGHDKMSLDPRVELEKRSLEYSRLRIQKVDVYDEGSYTCVQTHPEPKTSQV 124

QY 124 VTVLGIPOKPIITGVKSLREKDTATLNCOSGSKPAARLTWRKGDQELHGEPTRIQEDP 183
DB 125 YLIVQVPPKLSNSTDVTVNVEGNSVTLVCVANG-RPEPVITWR-----HLTPT----- 171

QY 184 NGKTFVSSSV--TFQVTRDDGASIVCSVNHESLKGADSTSORIEVLVTPAMIRPDP 241
DB 172 -GREFEGEVEEYLEILGITREQSG-KVECKAANE-VSSAD-VKQVKVTVNPPT-ITESKS 226

QY 242 PHREGOKLLHCEGRGNPVPOQYLWKE-----GSVPPLKMTQ-ESALIFPLNKS 294
DB 227 NEATTGQASLKCEASAVPAP-DFEYWRDTRTNSANGLEIKSTEGOSSLTVTNVTBEHY 285

QY 295 GTYGTCTATSNMGSYKAYITLNVNDPSPVPSSSYTHAIIIGI-VAFIVFLLIIMLIEL 351
DB 286 GNYTCVAANKLG-----VTNASLVLRPGRSVRGINGSISLAVPLWLLASLLCL 334

RESULT 12

JC5288

SHP substrate-1 protein, 509 - mouse

C;Species: Mus musculus (house mouse)

```

Db      47  GGTVELPCHLLPPTTERRVSVQVWRLDGTWAAFHPS-----FGVDFPNSQFSKORLSFV 101
QY      87  TSSTP-----HELISISINVALADEGEYTCSTFTMPVRTAKSLVTLVGLIPQKP--IITGV 138
Db      102  RARPETNADLRDATLAFRGLRVEDEGNCYCEFAFFNGTFRG-VTWLRVIAQENHAEQA 160
QY      139  KSLIREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDP-NGKTFVSSSVTFQ 197
Db      161  EVTIGSQSVAVARCVSTGGRPPARIW---ISLGGKADTQEPGAGTGTIISYSLV 217
QY      198  VTRDDGASIVCSVNHESLKGADRSTSQRIEVLVYPTAMIRPPHPREG-----Q 248
Db      218  PVGRADGVKVTCTVERHESPEE-----PILLPVTLSVRYPPEVSISGYDDNWLGRS 268
QY      249  KLLHHEGGRNPVPOQYLWE-KGSSVPLKQWQTESALIPFLNKSQSGTGTCTATSNMGS 307
Db      269  EAILTCDVRNPFPTDYDWTSGVFPASAVAGSQSLVSHSDRMVNTTFCIATNAVGT 328
QY      308  YKAYVTLNVNDPSPVPSSTYHAIIGVIAFTVFLILLMLIFLGHYLIIRHKGYTLTHEA 367
Db      329  GRAEQVILVRD---TFQASRDVGLVWAGVGLLVLLAGGLALILRGRRRRSPGG 385
QY      368  KGSDDAPDADTALINAEQSGSGDKKEYF 397
Db      386  GGND-----GDRGSYDPKTVQVF 402

RESULT 7
JC5519
S:Species: Gallus gallus (chicken)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 17-Nov-2000
C:Accession: JC5519
R:Hancock, K.A.; Gooley, A.A.; Jeffrey, P.L.
Mol. Brain Res. 44, 273-285, 1997
A:Title: AvGP50, a predominantly axonally expressed glycoprotein, is a member of the Igl
A:Reference number: JC5519; MUID:97225899; PMID:9073169
A:Accession: JC5519
A:Molecule type: mRNA
A:Residues: 1-338 <HAN>
A:Experimental source: brain
C:Comment: This protein belongs to the Iglon's subfamily of cell adhesion molecules.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: glycoprotein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-338/Product: 50K glycoprotein #status predicted <IM1>
F:146-199/Domain: immunoglobulin homology <IM2>
F:146-199/Domain: immunoglobulin homology <IM3>
F:232-292/Domain: immunoglobulin homology <IM3>
F:40,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 11.6%; Score 243; DB 2; Length 338;
Best Local Similarity 27.6%; Pred. No. 2.3e-10;
Matches 86; Conservative 44; Mismatches 152; Indels 30; Gaps 13;

QY      4  PAASLILLPACCAWPGGANLSQDQSPWTSDETVVAGTVLKCQVKDHEDSSLOWS 63
Db      7  PDRKQLPLVLLRLCLLPLGLPVRSDFTGRDNTITVRQDGTAILRCFVED-RSSKVAWL 65
QY      64  NPAQQTLYFGKRALRDNRILQVLTSTPHELISISINVALADEGEYTCSTFTMPVETAKSL 123
Db      66  N-RSGIIFAGEDKWSLDPRVELEKRSPLSEYSRIQKVDVYDEGTSVQTOHHPTKSOV 124
QY      124  VTVLGTPQKPIITGYKSLRREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDP 183
Db      125  YLIVQVPPKINSISSDITVNEGSNVLVCMANG-RPEPVITWR-----HLTFT----- 171
QY      184  NGKTFVSSSV--TFQVTRDDGASIVCSVNHESLKGADRSTSQRIEVLVYPTAMIRPPDP 241
Db      172  -GKEFGEEBEYLIGITREQSG-KYECKAANE-VASAD-VKQVRVTVNVPPT-ITESKS 226
QY      242  PHRREGQKLLHCEGRGNVPVQOYLWEKE-----GSVPLKMT-QESALIPFLNKSQDS 294

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Db      227  NEATGROALLPCEASAVPTP-DFEWYRDDTRINSANGLEIKSTGSQILLMVANVTSEHY 285
QY      295  GTYGTATSNMG 306
Db      285  GNYTCVAANKLG 297

RESULT 8
JC5287
SHP substrate-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC5287
R:Yamamoto, T.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A:Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
A:Reference number: JC5287; MUID:97223399; PMID:9070220
A:Contents: Brain
A:Accession: JC5287
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-503 <YAM>
A:Cross-references: DDBJ:D86043; NID:G1864010; PIDN:BAA12974.1; PID:G1864011
C:Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C:Genetics:
A:Gene: shps-1
A:Map position: 20p13

Query Match 11.6%; Score 241.5; DB 2; Length 503;
Best Local Similarity 25.2%; Pred. No. 4.8e-10;
Matches 106; Conservative 64; Mismatches 163; Indels 87; Gaps 20;

QY      8  LLLLLLACCAWPGGANLSQDQSPWTSDETVVAGTVLKCQVKDHEDSSSL-----Q 61
Db      14  LLLCLLAASCAWSGVAAGEELQVIQD-DKSVSVAAGESAILHCTV-----TSLIPVGPQI 67
QY      62  W---SNPAQQTLYFGKRALRDNRILQVLTSTPHE---LSISINVALADEGEYTCSTF-- 113
Db      68  WFRGAGPARELIY-NOKEGHFPRVTVTSESTKKNMDFISISNITPADAGTYCYCKFRK 126
QY      1-4  ---TMPVRTAKSLVTLVGLIPQKPIITGYKSLRREKDTATLNCQSSGSKPA-ARLTWRKG 168
Db      127  GSPDTEFKSAGTSLVRAKSPAPVSVGPAARATPQHTVSTFCTESHGFSRDIITLWFKN 186
QY      169  DQELHGEPTRIQEDPQNGK--TFTVSSSVTFQVTRDDGASIVCSVNHESLKGAD-RSTSQ 225
Db      187  GNELSDFTQNV--DPVGSVSYSIHTAKVLTREDVHVSQVCEVAHVTLQGDPLRGATN 244
QY      226  RIEVLVYPTAMIRDPDHPREGQKLLHCEGRG-NPVPQOYLWEKGSVPPLKMTQESAL 284
Db      245  LSETIRVPTLTQVTPVRAENQ--VNTCQVRKFPQRLQTLWLENGV---SRTEAST 300
QY      295  IFPELNKSDSGTGTCTATSNMGSYKAYITLVN-----NDPSVPS----- 324
Db      301  V-----TENKDTY-----NWSMLLVNVSAAHDDVKLTQCVHEDGQPAVSKSHDLK 347
QY      325  -----SSSTYHAIIGG-----IVAFIVFLILLMLIFLGHYLIIRHKGYTLTHEAKGS 370
Db      348  VSAHPKEQSGNTAAENTGSNERNIYVGVVCTLLVALLMAALYLVRIR-----QKKAQGS 403

RESULT 9
I68093
PRR2 delta - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I68093
R:Berberie, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I68093

```


A:Cross-references: EMBL:X64116; NID:g35809; PIDN:CRA45478.1; PID:g825708
A:Note: 67-Ala was also found
A:Note: the gamma form has 331-Gly and lacks residues 332-384
R:Wendelschohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A:Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and expression
A:Reference number: A90910; MUID:89168426; PMID:2538245
A:Accession: A31496
A:Molecule type: mRNA
A:Residues: 1-66, 'A', 68-417 <MEN>
A:Cross-references: GB:M29535
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
C:Genetics:
A:Gene: GDB:PVR; PVS
A:Cross-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F:21-343/Domain: extracellular #status predicted <EXT>
F:21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>
F:42-125/Domain: immunoglobulin homology <IMM1>
F:159-223/Domain: immunoglobulin homology <IMM2>
F:259-314/Domain: immunoglobulin homology <IMM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-417/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Disulfide bonds: #status predicted
F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 281; DB 1; Length 417;
Best Local Similarity 28.0%; Pred. No. 4.8e-13;
Matches 108; Conservative 50; Mismatches 158; Indels 70; Gaps 17;

QY 5 AASILLILLFACWAPGGANLSQDDSQPWTSETVA-----GGTVLKC--QVKD 54
DB 7 AAWPLLLVALLVLSWPP-----PGTGDVVVQAPQVPGFLGDSVTLPCYQVNP 55

QY 55 HE---DSLOWNSPAQTLVFEKRAL-----RDNIQLVTSTPHELISISIN 99
DB 56 MEVTHVSQLTWTR-----HGSGSNAVPHQTGSPYSSESKLLEFVAA---RLGAELRN 105

QY 100 VAL-----ADEGEYTCSTFTMPVTRAKSLVTLVGLPQKPIIFG--YKSLREKDTATL 150
DB 106 ASLRMFLGRVEDEGNYCTLFTVFP--QGSRSVDIWLRLAKPONTAEVQKVLQTPGVPM 164

QY 151 NCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPN--GKFTVSSSVTFQVTRDDGASIV 208
DB 165 RCVSTGGRPPAQITWH---SDLGMPNTSQV--PGFLSGVTVTLSLWILVSSQVDDGKNVT 220

QY 209 CSVNHESLKGADRTSQRIEVLYPTAMIRDPDPHPREGQ--KILLHCEGRGNPVPOQYLW 267
DB 221 CKVEHSEFEKQLIT--VNLITYYPPEVISGYDNNWYLGQNEALTCDARSNPETGVNW 279

QY 268 EKE--GSPVPLKMTQESALIFPLFNKSDGTYGCTATSNMGSYKAYITLVNNDPSPVSS 326
DB 280 STTWGPIPPFAVAGQAQLIRPVDKPIINTLTCNVNLTALGARQAELTVQVKEGPEHSG 339

QY 327 STYIAIGGIVAFIVFLLIMLIFLG 352
DB 340 MSRNAIL-----FLVGLVNLVLLLG 360

RESULT 5
A53437
poliovirus receptor mPVR - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A53437
R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with p

A:Reference number: A53437; MUID:94179228; PMID:8132569

A:Accession: A53437

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-530 <AOX>

A:Cross-references: GB:D56107; NID:g475017; PIDN:BAA05103.1; PID:g825507

A:Experimental source: C57BL/6, brain

A:Note: sequence extracted from NCBI backbone (NCBI:146664, NCBI:146667)

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 12.0%; Score 250; DB 2; Length 530;

Best Local Similarity 25.7%; Pred. No. 1.2e-10;

Matches 86; Conservative 49; Mismatches 145; Indels 54; Gaps 13;

2

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 11.5056 Seconds

(without alignments)
3327.442 Million cell updates/sec

Title: US-09-778-187B-10

Perfect score: 2086

Sequence: 1 MGAPAAALLLLLLLFACCA.....AIINAEGGSGGDKKEYFI 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	285.5	13.7	417	2 A44194	poliovirus recepto
2	284	13.6	392	2 B44194	poliovirus recepto
3	281	13.5	392	1 RWHUPD	poliovirus recepto
4	281	13.5	417	1 RWHUPA	poliovirus recepto
5	250	12.0	530	2 A53437	poliovirus recepto
6	248.5	11.9	467	1 HLMSP3	poliovirus recepto
7	243	11.6	338	2 JC5519	50K glycoprotein p
8	241.5	11.6	503	2 JC5287	SHP substrate-1 pr
9	228	10.9	538	2 I68093	PRR2 delta - human
10	225.5	10.8	583	2 I39428	alcam - human
11	225	10.8	338	2 JC4776	limbic-system-asso
12	224	10.7	509	2 JC5288	SHP substrate-1 pr
13	224	10.7	513	2 JC5289	SHP substrate-1 pr
14	221.5	10.6	518	2 JC4024	poliovirus recepto
15	221.5	10.6	702	2 A36319	carcinoembryonic a
16	218.5	10.5	739	2 JS0675	vascular cell adhe
17	218	10.5	5175	2 T20992	hypothetical prote
18	218	10.5	5198	2 T43290	hemictatin precurs
19	216.5	10.4	338	2 JC1238	opioid-binding pro
20	216	10.4	345	2 JC1239	opioid-binding pro
21	216	10.4	478	2 JS3960	PRR2 alpha - human
22	215	10.3	345	2 JC4025	opioid-binding cel
23	211	10.1	345	2 S03199	opioid-binding pro
24	210.5	10.1	1612	2 T30805	duttl protein - mo
25	209	10.0	4391	2 A38096	perlecan precursor
26	204.5	9.8	1651	2 T14160	transmembrane rece
27	204	9.8	344	2 JS6551	neurotrophin - rat
28	203.5	9.8	7962	2 I38346	elastic titin - hu
29	197.5	9.5	588	2 JH0506	adhesion molecule

30 197.5 9.5 588 2 A45254 surface glycoprote
31 195 9.3 402 2 T09062 probable advanced
32 194.5 9.3 3707 2 S18252 heparan sulfate pr
33 194 9.3 547 1 S28904 intercellular adhe
34 191.5 9.2 1427 2 I51669 tumor suppressor -
35 191 9.2 764 2 A49448 irregular chiasm C
36 190.5 9.1 646 2 I38049 cell surface glyco
37 189 9.1 407 2 T08732 hypothetical prote
38 188 9.0 628 2 I38000 Lutheran blood gro
39 187.5 9.0 523 2 I50478 neurulin - goldfis
40 187.5 9.0 4162 2 T42633 connectin/titin -
41 186 8.9 1241 2 T37190 nephrin - human
42 184 8.8 588 2 I37202 B-CAM protein - hu
43 183.5 8.8 584 2 I50419 s-glycerin precurs
44 182.5 8.7 416 2 A54017 colon carcinoma-as
45 182.5 8.7 587 2 JH0464 DM-GRASP precursor

ALIGNMENTS

RESULT 1

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C;Species: Cercopithecus aethiops (green monkey, grivet)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: A44194

R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A;Title: A second gene for the African green monkey poliovirus receptor that has no puta

A;Reference number: A44194; MUID:93059631; PMID:1331508

A;Accession: A44194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-417 <KOI>

A;Cross-references: GB:S48777

C;Superfamily: poliovirus receptor; immunoglobulin homology

C;Keywords: transmembrane protein

F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 13.7%; Score 285.5; DB 2; Length 417;
Best Local Similarity 26.2%; Pred. No. 2.3e-13;
Matches 112; Conservative 56; Mismatches 189; Indels 71; Gaps 17;

Qy	10	LLLLFACCAWAGGANSQDSQFWSDETVVA-----GGTVLKC--QVKDHD--	57
Db	12	LLLLLLELSWPP-----PGTGDIIVQAPTQVPGFLGDSVTLPCYLQVGMEEH	60
Qy	58	-SSIQWSNPAQ-----QTLYFGEKEALRDNRIQLVTSPTHELSISISNVALADEG	106
Db	61	VSQLTWSRHGSGSMVPHOTQGNYSERPRLEFVAARLGTIEL-RDASLRFGLRVEDEG	119
Qy	107	EYTCISFTMPVRVAKSLVTVLGIPOKEPIITG--YKSSLREKDTATLNCSSGSKPAARLT	164
Db	120	NYTCLFTFP--QGSRSVDIWLRLVLAKEQNTAEVKQVLTGKVPVAVCVSTGGPRPAHIT	178
Qy	165	WRKGDQBLHGEPRIQEDPN--GKFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRS	222
Db	179	WH---SDLGGMPTNSQA-PGFLSGTVTVTSILWILVPSQVDGKSVTKVEHSEPKQLL	234
Qy	223	TSQRIEVLVYPTAMIRP-DPPHPREGOKLLHCEGRGNVPVQQYLWEKE-GSVPLPKMTQ	280
Db	235	T-VNLTVYVPEVISIGYDNNWYLSQNEALITCDARNPEPTGNWMTWGPLEPFAVAQ	293
Qy	281	ESALIFPFLNKSQGTGCTATSNMGSYKAYTYTLNVND-PSPVPSSTSYHAITGIVAF	339
Db	294	GAQLLIPVDKPIINTTFCNVTNALGARQAEELTVQKEGPPSEPSGWS-----NIIF	347
Qy	340	IVFLLLLIMLIFLG-----HYLRHKGTYLTAEAKGSDDDAPDADTAIIN	382
Db	348	LILGIVILLTLIGIGVYFVRSRCSREELWCHLSPSSEEHASANGYISYSDVSREASS	407
Qy	333	AEQQSGG	390

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QY 356 VPSSSTY-----HAIIGGIVAFIVFLLIMLIFLGHY 388
Db 339 PPTTTTTTTTTTTTIIITDSRAGEGSIKRAVDHAVIGVAVVAVFAMLCCLLIILGRY 398
QY 389 LIRHKGTYLTHAKSGDDAPDADTAIINAEQSGGDDKKEYFI 432
Db 399 FARHKGTYFTHEAKGADDAADADTAIINAEQGNNSSEKKEYFI 442

RESULT 14
US-09-930-803-1
; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHUI770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-930-803-1

Query Match
Best Local Similarity 31.9%; Score 722; DB 4; Length 442;
Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;

QY 4 PAASLLLLILF-ACCWAPGAGNLSDGYWQEDLELGTPLAPLDEAISTVWSSPDMLAS 62
Db 22 PGLRLRLLLLFSAALIPGT-----DG-----QNL----- 47
QY 63 QDSQPTSDTIVVAGGTIVLKCQVQKHEDSSLOWNPAQOTLYFGKEKRALRDNRIQLVTS 122
Db 48 -----FTKDVTVIEGEVATISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLLNF 102
QY 123 TPELSISINVALADEGETCSIFTFMPTAKSLVTVLGIPOKPIITGYKSSLRKDTA 182
Db 103 SSELKVSUNVSIISDEGRYFCOLYTDPPQESYTIITVLVPPNLMIDIOKDTAVEGEEI 162
QY 183 TLNCQSGSKPAARLTWRKGDQELHGEPTIQEDPNEGKTFTVSSSVTFQVTRDDGASIV 242
Db 163 EVNCTAMASKPATIRFWKGNTELKKG-SEVEEWS--MYTVTSQMLKVKHEDDGVPI 219
QY 243 CSVNHSLKGADSTSRQIEVLYTPTAMIRDPDP-----HPREGQKLLHCEGRGNVPQQY 299
Db 220 QVEHPAVTG-NLQTRYLEBVQKQVHIQMTVPLQGLTREGDALELTCEAIGKQPVMV 278
QY 300 LWK-EGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYTINVDPS---P 355
Db 279 TWKVDDEMPQHAVLSGNLFINNLTNDGTIRCEASNIVGKAHSDYMLYVDDPTTIP 338
QY 356 VPSSSTY-----HAIIGGIVAFIVFLLIMLIFLGHY 388
Db 339 PPTTTTTTTTTTTTIIITDSRAGEGSIKRAVDHAVIGVAVVAVFAMLCCLLIILGRY 398
QY 389 LIRHKGTYLTHAKSGDDAPDADTAIINAEQSGGDDKKEYFI 432
Db 399 FARHKGTYFTHEAKGADDAADADTAIINAEQGNNSSEKKEYFI 442

RESULT 15
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1

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; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-778-510-22

Query Match
Best Local Similarity 31.6%; Score 715.5; DB 4; Length 423;
Matches 165; Conservative 75; Mismatches 140; Indels 77; Gaps 10;

QY 9 LLLLLLACCWAPGAGNLSDGYWQEDLELGTPLAPLDEAISTVWSSPDMLASQSQW 68
Db 10 LLLLLLSAALIPGT-----DG-----QNL-----F 30
QY 69 TSDETIVVAGGTIVLKCQVQKHEDSSLOWNPAQOTLYFGKEKRALRDNRIQLVTS 128
Db 31 TKDVTVIEGEVATISQVKNKSDSVIQLNPNRQTIYFRDPLKDSRFQLLNFSSSELK 90
QY 129 ISISNVALADEGETCSIFTFMPTAKSLVTVLGIPOKPIITGYKSSLRKDTATLNCS 188
Db 91 VSLTNVSIISDEGRYFCOLYTDPPQESYTIITVLVPPNLMIDIOKDTAVEGEEI 150
QY 189 SGSKPAARLTWRKGDQELHGEPTIQEDPNEGKTFTVSSSVTFQVTRDDGASIVNHE 248
Db 151 MASKPATIRFWKGNTELKKG-SEVEEWS--MYTVTSQMLKVKHEDDGVPIQVHEP 207
QY 249 SLKGADSTSRQIEVLYTPTAMIRDPDP-----HPREGQKLLHCEGRGNVPQQYLWEK-E 304
Db 208 AVTG-NLQTRYLEBVQKQVHIQMTVPLQGLTREGDALELTCEAIGKQPVMVTVRVD 266
QY 305 GSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYTINVDPS---PVPSSSS 361
Db 267 DEMPQHAVLSGNLFINNLTNDGTIRCEASNIVGKAHSDYMLYVDDPTTIPPTTIT 326
QY 362 TY-----HAIIGGIVAFIVFLLIMLIFLGHYLRHKG 394
Db 327 TTTTTTTTIIITDSRAGEGSIKRAVDHAVIGVAVVAVFAMLCCLLIILGRYPARHG 386
QY 395 TYLTHEAKSGDDAPDADTAIINAEQSGGDDKKEYF 431
Db 387 TYTTHEAKGADDAADADTAIINAEQGNNSSEKKEYF 423

Search completed: May 27, 2004, 09:36:58
Job time : 16.8018 secs

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QY 122 STPHLSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKEDT 181
 Db 91 ASWHELSISVSDLSDEGGYTCSLFTMPVKTSKAVTLVIGVEPKQISGFSPVMEGL 150
 QY 182 ATLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRDDGAS 241
 Db 151 MQLTCKTSGSKPAADIRFWKNDKEIKDVYKKEEDANRKTFTVSSTLDFRVDSDGVA 210
 QY 242 VCSVNHESLKADRSQRIEVLVYTPMTAMIRPDPHPHREGOKLLHCEGEGNVPQOYLW 301
 Db 211 ICVRDHESLNATQVAMQVLEIHYTPSVKIPSTPPFQEGQPIILTCESKGLPLBEVLW 270
 QY 302 EKEGSV---PPLKMTQESALIFPFLNKSQSGYGCATSNMGSYKAYYTLNVNDP 352
 Db 271 TKDGELPDPDRMVVSGRELNIPLNKTNGTYRCEATNIGQSSARYVLVHDVPTLL 330
 QY 353 PSPV-----PSSSTY-----HAIIGVAVIFVFL 378
 Db 331 PTTIISLTATVTTVAITTSPTTSATTSIRDPNALAGONGPDHALIGIVAVVFT 390
 QY 379 LIMLIFIGHYLRKHGTYLTHEAKGSDADPADTALINAEQSGGDDKKEYFI 432
 Db 391 LCSIFLLGRYLARKHGYLTNEAKGADPADTALINAEQSQVNABEKKKEYFI 444

RESULT 12
 US-09-866-028-61
 ; Sequence 61, Application US/09866028
 ; Patent No. 6642360
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tomas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548PIC1
 ; CURRENT APPLICATION NUMBER: US/09/866,028
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 61
 ; LENGTH: 440
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-866-028-61

Query Match 32.0%; Score 723.5; DB 4; Length 440;
 Best Local Similarity 36.2%; Pred. No. 7e-57;
 Matches 168; Conservative 74; Mismatches 145; Indels 77; Gaps 10;
 QY 3 APAASLLLLLLFACCAWAPGGANLSODGYWQEOLEGLTAPLDEAISSTVWSSPDLAS 62
 Db 20 APGLRLLLLLFSAALIPFG-----DG-----QNL----- 45
 QY 63 QDSQPWTSDETVAAGTGVVLKQVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLVTS 122
 Db 46 -----FTKDVTVIEGEVATISCVQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLN 100
 QY 123 TPHELSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKEDTA 182

Db 101 SSSELKVLSTNVISDEGRYFCQLYTDPQESYTTITVLVPPRNLMIDIQKTAVEGEI 160
 QY 183 TLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRDDGASIV 242
 Db 161 EYNCTAMASKPATIRFWKNTLKGK-SEVEWSD--MYTTSQMLKVKHEDDGVPI 217
 QY 243 CSVNHESLKADRSQRIEVLVYTPMTAMIRPDPHPHREGOKLLHCEGEGNVPQOYLW 299
 Db 218 CQVEHPAVTG-NLQTVLEVOYKQVHIQMTYPLQGLTREGDALELTCEAIGKPOVVMV 276
 QY 300 LWEK-EGSVPLKMTQESALIFPFLNKSQSGYGCATSNMGSYKAYYTLNVNDP---P 355
 Db 277 TWVRVDEMPQHAVLSGPNLFNNLNKTNGTYRCEASINVGKASDYMLYVDPPTIP 336
 QY 356 VPSSSTY-----HAIIGVAVIFVFL 378
 Db 337 PPTITTTTTTTTTITITSDRAGEBSIRAVDHAVIGGVAVVVFAMCLLIILGRY 396
 QY 389 LIHKGTYLTHEAKGSDADPADTALINAEQSGGDDKKEYFI 432
 Db 397 FARHKGTYFTHAKGADDAADATALINAEQSQVNABEKKKEYFI 440

RESULT 13
 US-09-778-510-20
 ; Sequence 20, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778,510
 ; CURRENT FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-778-510-20

Query Match 31.9%; Score 722; DB 4; Length 442;
 Best Local Similarity 36.4%; Pred. No. 9.6e-57;
 Matches 169; Conservative 74; Mismatches 143; Indels 78; Gaps 11;
 QY 4 PAASLLLLLLF-ACCWAPGGANLSODGYWQEOLEGLTAPLDEAISSTVWSSPDLAS 62
 Db 22 PGLRLRLLLLLFSAALIPFG-----DG-----QNL----- 47
 QY 63 QDSQPWTSDETVAAGTGVVLKQVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLVTS 122
 Db 48 -----FTKDVTVIEGEVATISCVQVNSDDSVIQLLNPNRQTIYFRDPLKDSRFQLN 102
 QY 123 TPHELSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKEDTA 182
 Db 103 SSSELKVLSTNVISDEGRYFCQLYTDPQESYTTITVLVPPRNLMIDIQKTAVEGEI 162
 QY 183 TLNCSSGSKPAARLTWRKGDQELHGEPTRIOEDPNGKFTVSSSVTFQVTRDDGASIV 242
 Db 163 EYNCTAMASKPATIRFWKNTLKGK-SEVEWSD--MYTTSQMLKVKHEDDGVPI 219
 QY 243 CSVNHESLKADRSQRIEVLVYTPMTAMIRPDPHPHREGOKLLHCEGEGNVPQOYLW 299
 Db 220 CQVEHPAVTG-NLQTVLEVOYKQVHIQMTYPLQGLTREGDALELTCEAIGKPOVVMV 278
 QY 300 LWEK-EGSVPLKMTQESALIFPFLNKSQSGYGCATSNMGSYKAYYTLNVNDP---P 355
 Db 279 TWVRVDEMPQHAVLSGPNLFNNLNKTNGTYRCEASINVGKASDYMLYVDPPTIP 338

Query Match	44.9%;	Score	1017.5;	DB	2;	Length	444;
Best Local Similarity	48.6%;	Pred. No.	2e-83;				
Matches	201;	Conservative	70;	Mismatches	100;	Indels	43; Gaps 4;
QY	62	SODSQPWTSDFTVWAGGTVVLKCVKQVHEDSSLOWNSPAQOTLTFGEKRALDRNRIQLVT	121				
Db	31	SOQQPFLQNTVVEGGTALLTCRDQNDNTSLQNSPAQOTLYPDDKKALDRNRIELVR	90				
QY	122	STPHSLISISNVALADEGEYTCSTFTWPTAKSLTVVLGIPQKPIITGVKSSUREKDT	181				
		::	::	::	::	::	::
		::	::	::	::	::	::
Db	91	ASWHSLISISVDLSDEQYTCSLFTWPKVTSKAYLTVLGVPKRPQISGFSPPWMEGDL	150				
		::	::	::	::	::	::
		::	::	::	::	::	::
QY	182	ATINCQSGSKPAARLTVWRKGDQELHGEPTRIQEDPENGKFTFTVSSSVTFQVTTREDDGASI	241				
		::	::	::	::	::	::
		::	::	::	::	::	::

```

RESULT 11
US-08-660-531-5
/ Sequence 5, Application US/08660531
/ Patent No. 6221645
/ GENERAL INFORMATION:
/ APPLICANT: Chrysler, Susanna M.S.
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Keim, Pamela S.
/ APPLICANT: Anderson, John P.
/ TITLE OF INVENTION: Beta-Secretase
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Ctr., 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/660,531
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/480,498
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heslin, James M.
/ REGISTRATION NUMBER: 29,541
/ REFERENCE/DOCKET NUMBER: 15270-002210US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-660-531-5

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Query Match	44.9%	Score 1017.5	DB 3	Length 444
Best Local Similarity	48.6%	Pred. NO. 2e-83		
Matches 201	Conservative 70	Mismatches 100	Indels 43	Gaps 4
62	SDSQPWTSDFTVAGGTWLKQVKHDESSLOWNSPAQQTLYFGKKALRDRNRILVLT	121		
31	SGQRPLONTVTVVGGTALITCRVDNDNTSLOWNSPAQQTLYFDDKKALRDRNRILVR	90		

RESULT 8

US-08-659-984A-1
 ; Sequence 1, Application US/08659984A
 ; Patent No. 5942400
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, John P.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Jacobson-Croak, Kirsten L.
 ; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 ; TITLE OF INVENTION: Inhibition
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/659,984A
 ; FILING DATE: 07-JUN-1996
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,152
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002810US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-659-984A-1

Query Match 44.9%; Score 1017.5; DB 2; Length 421;
 Best Local Similarity 48.6%; Pred. No. 1.9e-83;
 Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;
 Qy 62 SQDSQPTSDTETVAGTVVLCVKQVHEDSSLOWNSPAQOTLYFGKRALRDNRIQLVT 121
 Db 8 SQGQFPLTQNTVVEGGTAITLCRVQNDNTSLQNSPAQOTLYFDDKALRDNRIELVR 67
 Qy 122 STPHLSISISNVALADEGEYTCISFTMPVTRAKSLVTLGIPKPIITGVKSSLRKDT 181
 Db 68 ASWHLSISVSDVLSDEGQVTCSLFTMPVKTSKAYLTVLGVPEKPOISGFSFPMEGDL 127
 Qy 182 ATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKTFVSSVTFQVTRDDGASI 241
 Db 128 MQLTKTSGSKPAADIRFKNDEIKDVYKLEEDANKRTFTVSTLDFRDRSDDGAV 187
 Qy 242 VCSVNHSLSKGDRTSQRILEVLYPTAMIRPDPPHREGOKLLHCEGRGNVPVQYLW 301
 Db 188 ICRVDHESLNATPQVAMQVLEIHTYPSVKLIIPSTFPQEGQPLIITCSKKGKPLPEVLW 247
 Qy 302 EKEGVS---PPLKMTQESALIPFFLNKSDSGYGTATSNMGSKYKAYTYLNVND----- 352
 Db 248 TKDGGELPDRMVMVSGRELNLFLNKTNDNGTYRCEATNTIGSSAEYVLIHVDVENTILL 307
 Qy 353 PSFV-----PSSSTV-----HAIIGGIVATIVELL 378

Db 308 PTTIIPSLTATVTTTVAITTSPTTSIRDPNALAGQDPHALIGIVAVVFTV 367
 Qy 379 LIMLIFLGHYLRHKGYTLTHEAKGSDPADADTAIINAEGQSGDDDKCYFI 432
 Db 368 LCSIFLLGRLARHKGTYLTNEAKGAEDAPADTAIINAEGSQVNAEKKEFYI 421
 RESULT 9
 US-08-660-531-1
 ; Sequence 1, Application US/08660531
 ; Patent No. 6221645
 ; GENERAL INFORMATION:
 ; APPLICANT: Chrysler, Susanna M.S.
 ; APPLICANT: Sinha, Sukanto
 ; APPLICANT: Keim, Pamela S.
 ; APPLICANT: Anderson, John P.
 ; TITLE OF INVENTION: Beta-Secretase
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Ctr., 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,531
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/480,498
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Heslin, James M.
 ; REGISTRATION NUMBER: 29,541
 ; REFERENCE/DOCKET NUMBER: 15270-002210US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-326-2400
 ; TELEFAX: 415-326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 421 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-660-531-1

Query Match 44.9%; Score 1017.5; DB 3; Length 421;
 Best Local Similarity 48.6%; Pred. No. 1.9e-83;
 Matches 201; Conservative 70; Mismatches 100; Indels 43; Gaps 4;
 Qy 62 SQDSQPTSDTETVAGTVVLCVKQVHEDSSLOWNSPAQOTLYFGKRALRDNRIQLVT 121
 Db 8 SQGQFPLTQNTVVEGGTAITLCRVQNDNTSLQNSPAQOTLYFDDKALRDNRIELVR 67
 Qy 122 STPHLSISISNVALADEGEYTCISFTMPVTRAKSLVTLGIPKPIITGVKSSLRKDT 181
 Db 68 ASWHLSISVSDVLSDEGQVTCSLFTMPVKTSKAYLTVLGVPEKPOISGFSFPMEGDL 127
 Qy 132 ATLNCQSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGKTFVSSVTFQVTRDDGASI 241
 Db 128 MQLTKTSGSKPAADIRFKNDEIKDVYKLEEDANKRTFTVSTLDFRDRSDDGAV 187
 Qy 242 VCSVNHSLSKGDRTSQRILEVLYPTAMIRPDPPHREGOKLLHCEGRGNVPVQYLW 301
 Db 188 ICRVDHESLNATPQVAMQVLEIHTYPSVKLIIPSTFPQEGQPLIITCSKKGKPLPEVLW 247

Db 30 ---DSQPWTSDETVAGGVVLKCOVKHEDSSLOWNSPAQOTLYFGKGRALRDNRIQLV 86
Qy 121 TSTPHLSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKED 180
Db 87 SSTPHLSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRK 146
Qy 181 TATLNCQSSGSPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGAS 240
Db 147 TATLNCQSSGSPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDG 206
Qy 241 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGOKLLHCEGRGNPVPQYL 300
Db 207 IVCSNVHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGOKLLHCEGRGNPVPQ 266
Qy 301 WEKESGVPPLKMTQESALIPFPLNKSDSGTYGCTATSNMGSKYKAYTTLNNDPSPV 360
Db 267 WEKESGVPPLKMTQESALIPFPLNKSDSGTYGCTATSNMGSKYKAYTTLNNDPSP 326
Qy 361 STVHTAIGGVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAE 420
Db 327 STVHTAIGGVAFIVFLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAE 386
Qy 421 QSGGDDKKEYFI 432
Db 387 QSGGDDKKEYFI 398

RESULT 7

US-09-205-258-947
; Sequence 947, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 947
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-205-258-947

Query Match 52.5%; Score 1189; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.4e-99;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 ELSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKDTATLN 185
Db 1 ELSISINVALADEGEYTCISFTMPVRTAKSLVTLVGIPOKPIITGYKSSLRKDTATLN 60
Qy 186 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSV 245
Db 61 CQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSV 120
Qy 246 NHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGOKLLHCEGRGNPVPQOYLWEKEG 305
Db 121 NHESLKGADRTSQRIEVLYTPTAMIRPDPPHREGOKLLHCEGRGNPVPQOYLWEKEG 180
Qy 306 SVPLPKMTQESALIPFPLNKSDSGTYGCTATSNMGSKYKAYTTLNND 352
Db 181 SVPLPKMTQESALIPFPLNKSDSGTYGCTATSNMGSKYKAYTTLNND 227

RESULT 5
 US-09-778-187b-84
 ; Sequence 84, Application US/09902775A
 ; Patent No. 6686451
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, A.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth, J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/902.775A
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 60/146,222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944
 ; PRIOR FILING DATE: 1999-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 84

; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-902-775A-84
 Query Match 90.9%; Score 2059; DB 4; Length 398;
 Best Local Similarity 92.1%; Pred. No. 1.6e-177;
 Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
 QY 1 MGAPAAASLLILLFACCCWAPGGANLSQDGYWQBDLELGTALPLDEALISSTVWSSPDML 60
 Db 1 MGAPAAASLLILLFACCCWAPGGANLSQD----- 29
 QY 61 ASQDSQPWTSDETVVAGTWWLKQVCKHEDSSLOWNSPAQQTLYFGEKRALRDNRQLV 120
 Db 30 ----DSQFWTSDETVVAGTWWLKQVCKHEDSSLOWNSPAQQTLYFGEKRALRDNRQLV 86
 QY 121 TSTPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTLVGLIPQKPIITGYKSSLRKD 180
 Db 87 TSTPHELSSISNVALADEGEYTCSTFTMPVRTAKSLVTLVGLIPQKPIITGYKSSLRKD 146
 QY 181 TATLNCSSGSKPAARLTWRKGDQELHGPETRIQEDPNGKFTVSSSVTFQVTRDDGAS 240
 Db 147 TATLNCSSGSKPAARLTWRKGDQELHGPETRIQEDPNGKFTVSSSVTFQVTRDDGAS 206
 QY 241 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 300
 Db 207 IVCSVNHESLKGADRSQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 266
 QY 301 WEKEGVPPLKMTQESALIFPPFLNKSDSGTYGCTATSNMGSKYKAYITLVNDSPVPSS 360
 Db 267 WEKEGVPPLKMTQESALIFPPFLNKSDSGTYGCTATSNMGSKYKAYITLVNDSPVPSS 326
 QY 361 STTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAE 420
 Db 327 STTHAIIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTHEAKGSDDAPDADTAIINAE 386
 QY 421 QSGGDDKKKEYFI 432
 Db 387 QSGGDDKKKEYFI 398
 RESULT 6
 US-09-778-510-4
 ; Sequence 4, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778,510
 ; CURRENT FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 398
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-778-510-4
 Query Match 86.4%; Score 1955; DB 4; Length 398;
 Best Local Similarity 87.5%; Pred. No. 3.8e-168;
 Matches 378; Conservative 11; Mismatches 9; Indels 34; Gaps 1;
 QY 1 MGAPAAASLLILLFACCCWAPGGANLSQDGYWQBDLELGTALPLDEALISSTVWSSPDML 60
 Db 1 MGAPAAASPVPLILLLLACSWAPGGANLSQD----- 29
 QY 61 ASQDSQPWTSDETVVAGTWWLKQVCKHEDSSLOWNSPAQQTLYFGEKRALRDNRQLV 120

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Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
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Db 1 MGAPASLHLLHLLFACCPAGGANSOD-----29
Qy 61 ASODSQPWTSDTAVAGTTLVKQVQKDHEDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 120
Db 30 ---DSQPWTSDTAVAGTTLVKQVQKDHEDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 86
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Db 87 TSTPHELISISINVALADEGEYTCISFTMPVPTAKSLVTLVGIPOKPIITGYKSSLRKD 146
Qy 181 TATLNCSSGSKPAARLTWRKQDOELHGEPTRIQEDNGKTFVSSSVTQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKQDOELHGEPTRIQEDNGKTFVSSSVTQVTRDDGAS 206
Qy 241 IVCSVNHESLKGDARSTQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 300
Db 207 IVCSVNHESLKGDARSTQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 266
Qy 301 WEKESVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 360
Db 267 WEKESVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 326
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Db 327 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDAPDADTAINAEGG 386
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Db 387 QSGGDDKKKEYFI 398

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RESULT 4

US-09-905-125A-84
; Sequence 84, Application US/0905125A
; Patent No. 6664376

GENERAL INFORMATION:

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/05125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-84

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Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-177;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;
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Db 1 MGAPASLHLLHLLFACCPAGGANSOD-----29
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Db 30 ---DSQPWTSDTAVAGTTLVKQVQKDHEDSSLOWSNPAQOTLYFGEKRALDRNRIQLV 86
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Db 87 TSTPHELISISINVALADEGEYTCISFTMPVPTAKSLVTLVGIPOKPIITGYKSSLRKD 146
Qy 181 TATLNCSSGSKPAARLTWRKQDOELHGEPTRIQEDNGKTFVSSSVTQVTRDDGAS 240
Db 147 TATLNCSSGSKPAARLTWRKQDOELHGEPTRIQEDNGKTFVSSSVTQVTRDDGAS 206
Qy 241 IVCSVNHESLKGDARSTQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 300
Db 207 IVCSVNHESLKGDARSTQRIEVLVYPTAMIRDPDPHREGQKLLHCEGRGNPVPQOYL 266
Qy 301 WEKESVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 360
Db 267 WEKESVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVNDSPVPSS 326
Qy 361 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDAPDADTAINAEGG 420
Db 327 STYHAIIGGIVAFIVFLLHLLMFLGHYLRHKGTYLTHEAKGSDDDAPDADTAINAEGG 386
Qy 421 QSGGDDKKKEYFI 432
Db 387 QSGGDDKKKEYFI 398

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QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHKAGSDDDADDTAIINAEGG 420
DB 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHKAGSDDDADDTAIINAEGG 420
QY 421 QSGGDDKKEYFI 432
DB 421 QSGGDDKKEYFI 432

RESULT 2
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778.510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred No. 1.6e-177;
Matches 398; Conservative 0; Mismatches 0; Indels 34; Gaps 1;

QY 1 MGAPAAALLLLLLFACCAWPGGANLSQDGYWQEQDLELGTIAPLDEIAISVTWSSPDM 60
DB 1 MGAPAAALLLLLLFACCAWPGGANLSQD----- 29

QY 51 ASQDSQPMSTDETAVAGTAVLVKQVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLV 120
DB 30 ---DSQPMSTDETAVAGTAVLVKQVKDHEDSSLOWSNPAQOTLYFGKRALRDNRIQLV 86

QY 121 TSTPHELSISINVALADEGYTCISFTMPVRTAKSLVTLGIPKPIITGYKSSLREKD 180
DB 87 TSTPHELSISINVALADEGYTCISFTMPVRTAKSLVTLGIPKPIITGYKSSLREKD 146

QY 181 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQBDPNKGTFTVSSSVTFQVTRDDGAS 240
DB 147 TATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQBDPNKGTFTVSSSVTFQVTRDDGAS 206

QY 241 IVCSVNHESLKGADRTSQRILEVLTPTAMIRPDPPHREGOKLLHCEGRGNVPVQOYL 300
DB 207 IVCSVNHESLKGADRTSQRILEVLTPTAMIRPDPPHREGOKLLHCEGRGNVPVQOYL 266

QY 301 WEKEGVPPLKMTQBSALIFPFLNKSQGTGCTATSNMGSKYKAYTTLNVNDPSVPSS 360
DB 267 WEKEGVPPLKMTQBSALIFPFLNKSQGTGCTATSNMGSKYKAYTTLNVNDPSVPSS 326

QY 361 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHKAGSDDDADDTAIINAEGG 420
DB 327 STYHAIIGGIVAFIVFLLIMLIFLGHYLRHKGTYLTHKAGSDDDADDTAIINAEGG 386

QY 421 QSGGDDKKEYFI 432
DB 387 QSGGDDKKEYFI 398

RESULT 3
US-09-907-794A-84
; Sequence 84, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-84

Query Match 90.9%; Score 2059; DB 4; Length 398;
Best Local Similarity 92.1%; Pred. No. 1.6e-177;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 09:27:50 ; Search time 15.8018 Seconds
(without alignments)
1411.387 Million cell updates/sec

Title: US-09-778-187B-8

Perfect score: 2264

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2264	100.0	432	4	US-09-778-510-2
2	2059	90.9	398	4	US-09-778-510-6
3	2059	90.9	398	4	US-09-778-794A-84
4	2059	90.9	398	4	US-09-903-125A-84
5	2059	90.9	398	4	US-09-902-775A-84
6	1955	86.4	398	4	US-09-778-510-4
7	1189	52.5	227	4	US-09-205-258-947
8	1017.5	44.9	421	2	US-08-659-984A-1
9	1017.5	44.9	421	3	US-08-660-531-1
10	1017.5	44.9	444	2	US-08-659-984A-5
11	1017.5	44.9	444	3	US-08-660-531-5
12	723.5	32.0	440	4	US-09-866-028-61
13	722	31.9	442	4	US-09-778-510-20
14	722	31.9	442	4	US-09-930-803-1
15	715.5	31.6	423	4	US-09-778-510-22
16	342	15.1	65	4	US-09-205-258-949
17	319	14.1	58	4	US-09-205-258-950
18	317	14.0	64	4	US-09-205-258-948
19	310	13.7	64	4	US-09-205-258-361
20	280	12.4	52	4	US-09-205-258-951
21	249.5	11.0	393	1	US-08-423-742-2
22	242	10.7	388	1	US-08-423-742-4
23	239	10.6	517	4	US-09-723-368-4
24	238.5	10.5	503	4	US-08-999-689A-6
25	234	10.3	408	4	US-09-724-864-62
26	233	10.3	44	4	US-09-205-258-953
27	228.5	10.1	458	4	US-09-435-956A-1

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28 221.5 9.8 518 4 US-09-919-172-20
29 216.5 9.6 698 2 US-08-602-725-36
30 216.5 9.6 734 2 US-08-389-459A-17
31 216.5 9.6 734 3 US-08-987-867A-17
32 216.5 9.5 642 1 US-08-217-299-1
33 214.5 9.3 582 4 US-09-703-705-334
34 211.5 9.3 582 4 US-09-736-457-334
35 211.5 9.3 582 4 US-09-614-124B-334
36 211.5 9.3 582 4 US-09-671-325-334
37 211.5 9.3 582 4 US-09-589-184-334
38 210.5 9.3 583 2 US-08-432-016-2
39 210.5 9.3 583 2 US-08-684-594-2
40 209.5 9.3 479 4 US-09-723-368-2
41 208 9.2 338 2 US-08-414-657D-60
42 208 9.2 338 4 US-09-133-080-8
43 208 9.2 1651 3 US-09-540-245A-18
44 205.5 9.1 310 2 US-08-414-657D-45
45 205.5 9.1 338 2 US-08-414-657D-42

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ALIGNMENTS

RESULT 1

US-09-778-510-2

; Sequence 2, Application US/09778510

; Patent No. 6512095

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter

; TITLE OF INVENTION: Molecules Designated B7L1

; FILE REFERENCE: 2844-US

; CURRENT APPLICATION NUMBER: US/09/778,510

; CURRENT FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: PCT/US99/17906

; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: 60/095,663

; PRIOR FILING DATE: 1998-08-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 432

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-778-510-2

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Query Match 100.0%; Score 2264; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 5.5e-196;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MGAPAAASLLLLLLPACCCWA	PGGANLSQDGYWQDLELGTIAPLDEA	ISSTVWSSPDML	60
QY	51	ASQDSQPWTSDETVVAGT	VVVKQVQKHDESSLOWSNPAQO	TLVFGKRALRNRQLV	120
DB	51	ASQDSQPWTSDETVVAGT	VVVKQVQKHDESSLOWSNPAQO	TLVFGKRALRNRQLV	120
QY	121	TSTPHELSISINVALADE	GEYTCISITMPVRTAKSLVTL	VGIPQKPIITGYKSSLRKD	180
DB	121	TSTPHELSISINVALADE	GEYTCISITMPVRTAKSLVTL	VGIPQKPIITGYKSSLRKD	180
QY	181	TATLNCSSSKPAARLTWR	KQDELGEPTQEDNGKFTVSS	SVTQVTRDDGAS	240
DB	181	TATLNCSSSKPAARLTWR	KQDELGEPTQEDNGKFTVSS	SVTQVTRDDGAS	240
QY	241	IVCSVNHESLKGADRST	SQRIEVLVYTTAMRPPPHR	EGOKLLHCEGRGNVPOOYL	300
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DB	301	WEKEGVPPLKMTQESAL	IFPFLNKSDSGTGCTATSN	MGSYKAYITLVNDPSPVSSS	360